CRFE

From: Ramirez, Delia
Sent: ⁊⁸⁷ᵒ¹   Tuesday, January 18, 2005 1:06 PM
To: STIC-Biotech/ChemLib
Subject: case 09/459,573

Hi,

I would like to request the following interference search: SEQ ID NO:10 in the protein and nucleic acid databases.

Thank you,
                                                    ⁊⁊3ᴬᴬ

_____
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Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
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Alexandria, VA 22314
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***********************        ***********************        ***********************
STAFF USE ONLY                     Type of Search          Vendors and cost where applicable
                             NA Sequence: #_____         STN:_____
Searcher:_____        AA Sequence :#_____         DIALOG:_____
Searcher Phone: 2-           Structure: #_____         QUESTEL/ORBIT:_____
Date Searcher Picked up:____ Bibliographic:_____       LEXIS/NEXIS:_____
Date Completed:_____    Litigation:_____       SEQUENCE SYSTEM:_____
Searcher Prep/Rev. Time:___  Patent Family:_____         WWW/Internet:_____
Online Time:_____      Other:_____        Other(Specify):_____
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Date completed: _____	**Search Site**	**Vendors**
Searcher: ___Beverly e 2528___	_____ STIC	_____ IG
Terminal time: _____	_____ CM-1	_____ STN
Elapsed time: _____	_____ Pre-S	_____ Dialog
CPU time:_____	**Type of Search**	_____ APS
Total time: _____	_____ N.A. Sequence	_____ Geninfo
Number of Searches: _____	_____ A.A. Sequence	_____ SDC
Number of Databases: _____	_____ Structure	_____ DARC/Questel
	_____ Bibliographic	____Other C G N

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:        January 25, 2005, 16:33:23  ; Search time 40 Seconds
                                            (without alignments)
                                   369.723 Million cell updates/sec

Title:         US-09-459-573-10
Perfect score: 1135
Sequence:      1 MMQLVHLFMDEITMDPLHAV.........IGAIIGVFALRLIYEGVTQR 223

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters:    478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued_Patents_AA:*
         1: /cgn2_6/pcdata/1/iaa/5A_COMB.pep:*
         2: /cgn2_6/pcdata/1/iaa/5B_COMB.pep:*
         3: /cgn2_6/pcdata/1/iaa/6A_COMB.pep:*
         4: /cgn2_6/pcdata/1/iaa/6B_COMB.pep:*
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         6: /cgn2_6/pcdata/1/iaa/backfiles1.pep:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                            SUMMARIES
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Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	270	23.8	217	4	US-09-489-039A-8076	Sequence 8076, Ap
2	260	22.9	249	4	US-09-328-352-5813	Sequence 5813, Ap
3	245.5	21.6	269	4	US-09-489-039A-7320	Sequence 7320, Ap
4	237.5	20.9	214	4	US-09-328-352-6695	Sequence 6695, A
5	226	19.9	216	4	US-09-252-991A-18666	Sequence 18866, A
6	224	19.7	219	4	US-09-489-039A-7731	Sequence 7731, Ap
7	221	19.5	226	4	US-09-252-991A-31610	Sequence 31610, A
8	220.5	19.4	210	4	US-09-328-352-4775	Sequence 4775, Ap
9	220.5	19.4	235	4	US-09-328-352-8249	Sequence 8249, A
10	207	18.2	260	4	US-09-252-991A-25992	Sequence 25992, A
11	190.5	16.7	228	4	US-09-489-039A-8849	Sequence 8849, Ap
12	190	16.7	231	4	US-09-543-681A-4854	Sequence 4854, Ap
13	186	16.4	206	4	US-09-328-352-4784	Sequence 4784, Ap
14	182	16.0	208	4	US-09-328-352-5111	Sequence 5111, Ap
15	179	15.8	210	4	US-09-710-279-708	Sequence 708, App
16	179	15.8	224	3	US-09-134-001C-4608	Sequence 4608, Ap
17	176	15.5	237	4	US-09-252-991A-27175	Sequence 27175, A
18	173.5	15.3	211	4	US-09-489-039A-9608	Sequence 9608, Ap
19	167	14.7	214	4	US-09-489-039A-9793	Sequence 9793, Ap
20	166.5	14.7	228	4	US-09-252-991A-23837	Sequence 23837, A
21	165	14.5	241	4	US-09-328-352-7159	Sequence 7159, Ap
22	164	14.4	222	4	US-09-252-991A-26644	Sequence 26644, A
23	156.5	13.8	213	4	US-09-252-991A-16947	Sequence 16947, A
24	150.5	13.3	214	4	US-09-543-681A-4972	Sequence 4972, Ap
25	144.5	12.7	250	4	US-09-543-681A-4487	Sequence 4487, Ap
26	143	12.6	277	4	US-09-252-991A-23018	Sequence 23018, A
27	139	12.2	213	4	US-09-489-039A-11845	Sequence 11845, A
28	135.5	11.9	212	4	US-09-543-681A-4767	Sequence 4767, Ap
29	135	11.9	210	4	US-09-328-352-6808	Sequence 6808, Ap
30	130.5	11.5	240	4	US-09-328-352-7537	Sequence 7537, Ap
31	129.5	11.4	214	4	US-09-489-039A-8066	Sequence 8066, Ap
32	126.5	11.1	205	3	US-09-396-357-2	Sequence 2, Appli
33	126	11.1	211	4	US-09-252-991A-20747	Sequence 20747, A
34	114	10.0	220	4	US-09-328-352-4903	Sequence 4903, Ap
35	112.5	9.9	220	4	US-09-543-681A-4545	Sequence 4545, Ap
36	112	9.9	205	4	US-09-489-039A-12661	Sequence 12661, A
37	110	9.7	209	4	US-09-328-352-8225	Sequence 8225, Ap
38	110	9.7	211	4	US-09-543-681A-6708	Sequence 6708, Ap
39	108	9.5	221	4	US-09-328-352-6659	Sequence 6659, Ap
40	106	9.3	222	4	US-09-328-352-6471	Sequence 6471, Ap
41	98.5	8.7	211	4	US-09-489-039A-10442	Sequence 10442, A
42	96	8.5	325	4	US-09-489-039A-8024	Sequence 8024, Ap
43	94	8.3	214	4	US-09-328-352-6025	Sequence 6025, Ap
44	94	8.3	232	4	US-09-252-991A-24479	Sequence 24479, A
45	93.5	8.2	153	2	US-08-476-254-7	Sequence 7, Appli

```
                            ALIGNMENTS

RESULT 1
US-09-489-039A-8076
; Sequence 8076, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE:  2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE:  2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 8076
;   LENGTH: 217
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8076

Query Match             23.8%;  Score 270;  DB 4;  Length 217;
Best Local Similarity   28.8%;  Pred. No. 6.3e-22;
Matches   64;  Conservative   51;  Mismatches   89;  Indels   18;  Gaps    4;

Qy      4 LVHLFMDEITMDPLHAVYLTVGL-FVITFPNPGANLFVVVQTSLASGRRAGVLTGLGVAL  62
            | ||:|| ::||| |:|:  ::|||| :  |  |: ||| :|   ||::  |:
Db      2 LSSLFSCELTMLML--FLTVALVHIIALMSPGDFFFVSQTAISRSRREAMMGVLGITC  58

Qy     63 GDAFYSGLGLFGLATLITQCEEIFSLRIVGGAYLLMFAWCSMR------RQSTPQMS 114
            |    |  |:|    ||||| :|:   || |:|  :::|              ::
Db     59 GVMWAGVALLGLNLILARMAWLHNIIMVGGGLYLCWMGYQMLRGALKKETVASAEPQVE 118

Qy    115 TLQQPISAPWYVFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASI 174
            |::   ::| :|:  ::|: |||  |: :| :||| |  |:  |  |:  | : :|::|
Db    119 LARSGRS------FVKGLLTNLANPKAIIYFGSVFSLFVGDSVGAGARWGIFLLIIVETL 172

Qy    175 IWRVFLSQAFSLPAVRRAYGRMQRVASRVIGAIIGVFALRLI 216
            || | | ||:| |   :|  | |:    : ::  |  :|
Db    173 AWFMVVASLFALPGMRRGYQRMAKWIDGIAGTLPAGFGIHLI 214

RESULT 2
US-09-328-352-5813
; Sequence 5813, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
```

; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5813
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5813

Query Match   22.9%; Score 260; DB 4; Length 249;
Best Local Similarity   29.8%; Pred. No. 9.7e-21;
Matches   61; Conservative   47; Mismatches   85; Indels   12; Gaps   4;

Qy   22 LTVGLFVITFFN------PGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGL 75
Db   44 MLVALITLAFIHFCALITPGPDFFLVSQTAVSRSRKEAMLVVAGITVGVMFWASLALMGL 103

Qy   76 ATLITQCEEIFSLIRIVGGAYLLWFAWCSMR----RQSTPQMSTLQQPISAPWYVFFRRG 131
Db   104 NIIFEKMAWLKQGLLIAGGLYLCWLGYQMLRSAFSKNQQEVTTVELP-KAP-YLFFMKG 161

Qy   132 LITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASIIWRVFLSQAFSLPAVRR 191
Db   162 LLTNLSNPKAVIYFGSVSLFLANPQLDQVHWLLFFIVSVETIIWFCFVTFIFSLPSFRA 221

Qy   192 AYGRMQRVASRVIGAIIGVFALRLI 216
Db   222 AYRNFSKWIDIGISGGIFTVFGIFLI 246

RESULT 3
US-09-489-039A-7320
; Sequence 7320, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NO 7320: 14342
; SEQ ID NO 7320
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7320

Query Match   21.6%; Score 245.5; DB 4; Length 269;
Best Local Similarity   29.7%; Pred. No. 4.4e-19;
Matches   63; Conservative   37; Mismatches 101; Indels   11; Gaps   3;

Qy   17 LHAVYLTVGLFVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLA 76
Db   63 LSSLMAIAAVLIMGVISPGPSFIFVARNAVARSRLHGMVTALGTGAGAAIFSIMAMLGLQ 122

Qy   77 TLITQCEEIFSLIRIVGGAYLLWFAWCSMRRQSTP-QMSTLQQPISAPWYVFFRRGLITD 135
Db   123 KVLIAVPELFIGLRKVAGGLYLLWLIGYKIFRGSAQPMDFSASGMAGNRSLLKTFRDGLYTQ 182

Qy   136 LSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIV-----LASIIWRVFLSQAFSLPAVR 190
Db   183 LSNPKTALVFASIPTALLPAQIPT-----AFYYIVPLMSFLIDVSWYSLVALVLSADHPR 237

Qy   191 RAYGRMQRVASRVIGAIIGVFALRLIYEBGVTQ 222
Db   238 RVLRLKRRIDIATATVLGALGLRLIATSLTR 269

RESULT 4
US-09-328-352-6695

; Sequence 6695, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6695
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6695

Query Match   20.9%; Score 237.5; DB 4; Length 214;
Best Local Similarity   29.5%; Pred. No. 2.5e-18;
Matches   59; Conservative   42; Mismatches   96; Indels   3; Gaps   2;

Qy   21 YLTVGLF-VITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLGLATLI 79
Db   11 FLTLALIHFMAVILPGPDFVITVRQSVRGYLIGCLTAIGIGVGISVHVFYTLVGIGFLI 70

Qy   80 TQCEEIFSLIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPISAPWYVF--FRRGLITDLS 137
Db   71 QQSEWLMSLLRTAGAAYLVYLGWQCLRSQPNTNIEINGQLDSDTPSLFKAFTMGFLTNAL 130

Qy   138 NPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASIIWRVFLSQAFSLPAVRRAYGRMQ 197
Db   131 NPKATIFFLAIFTTIVSTTTPMKVQVFYGVWMCMVNAIWFMVVSVLPAQPIVRKRFLEFG 190

Qy   198 RVASRVIGAIIGVFALRLIY 217
Db   191 VYFERVMGVLLIGIALRLIW 210

RESULT 5
US-09-252-991A-18666
; Sequence 18666, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18666
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18666

Query Match   19.9%; Score 226; DB 4; Length 216;
Best Local Similarity   29.4%; Pred. No. 4.7e-17;
Matches   58; Conservative   43; Mismatches   90; Indels   6; Gaps   3;

Qy   21 YLTVGLFVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLGLATLIT 80
Db   19 FLTI--TVLAVISPGADFAMVSRNSLLYSRRAGLLTALGIGAGVTVHVGYSIIGLGVGVVR 76

Qy   81 QCEEIFSLIRIVGGAYLLWFAWCSM--RRQSTPQMSTLQQPISAPWYVFFRRGLITDLSN 138
Db   77 ESLALFTALKLAGAAYLVFLGLRMLLAREDSVAEEAAGGAGVSS--WAMLRSGFLTNALN 134

Qy   139 PQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASIIWRVFLSQAFSLPAVRRAYGRMQR 198

Wed Jan 26 08:14:33 2005

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Db  135 PKTCLFVVSLFMQVIDPHTALPAQLGYGAFIALAHVAWFGLVACFLSSPAVRGRILLRFRR 194

Qy  199 VASRVIGAIIGVFALRL 215

Db  195 RIDQFFGALLVGFGVLL 211
```

RESULT 6
US-09-489-039A-7731
; Sequence 7731, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.20040001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7731
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7731

Query Match   19.7%;   Score 224; DB 4;   Length 219;
Best Local Similarity   30.7%;   Pred. No. 8.1e-17;
Matches   63; Conservative   39; Mismatches   89; Indels   14; Gaps   6;

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Qy   18 HAVYLTVGLFVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLAT  77
        :  ||:||  :||  :   |:  |||:::||  |||   |  |    |  ||  ::|
Db   17 YLTYLIVGAVFIIIV--PGPNTFFVLKTGIAHGVKKGYLAAAGVFIGDAVLMFLAFAGVAT  74

Qy   78 LITQCEEIFSLIRIVGGAYLLWFA---WCSMRRQSTPQMSTLQQPISAPWYVFFRRGLIT 134
        ||  |  ::   |   | ||  ::|      |:  :||::|  ::||  |   :   ||  ||
Db   75 LIKTTPVLFNVVRYLGAIYLLWLGGKMLYAVLTQRDGQSDASAEPASA----ILKRSLTL 130

Qy  135 DLSNPQTVLFFISIF--SVTLNAETPTWARLMAWAGIVLASIIWRVF--LSQAFSLPAVR 190
         |  ::||   ||:|  |   :|:  :||  |  ||  |  :|  ||   ::|       |  ||
Db  131 SLTNPKAILFYVSFFVQFIDVNAKTPGVAFFILALTLEVISFCYMSFLIILSGSFVTRYV- 189

Qy  191 RAYGRMQRVASRVIGAIIGVFALRL 215
         ||   |:   |  |  ||  |  |
Db  190 KTRKKLAKLGNSLIGLVFVGFAARL 214
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RESULT 7
US-09-252-991A-31610
; Sequence 31610, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31610
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31610

Query Match   19.5%;   Score 221; DB 4;   Length 226;
Best Local Similarity   27.2%;   Pred. No. 1.8e-16;
Matches   55; Conservative   46; Mismatches   85; Indels   16; Gaps   6;

```
Qy   18 HAVYLTVGLFVIT----FFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGL  72
        :  ||:||  :||:||  |::||::|   |:|::
Db   20 YRIMLETSLFVATLATLGMLSPGPDFFLIIRNAARYQRSAAMMTSLGVILGVATHMAYCV  79

Qy   73 FGLATLITQCEEIFSLIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPIS----APWYVF 127
        ||| |||   |   ||  | |||||||    | :||  || | :|||      APWYVF
Db   80 AGLAVLITTTPWLFNALKYTGAVYLIWIGIQALRSRGG---GTILDLAVGGVQRVGHWSAF 136

Qy  128 FRRGLITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLA-SIIWRVFLSQAFSL 186
        |:||:|  :| ::|||  :::|  ::  |:|||||  || |  |  :  :  |||::|
Db  137 L-QGYLCNLLNPKATLFFLAVFTQVLSLDS-SFAEKLWYAGIIVGLAALWWPLLVVLIQS 194

Qy  187 PAVRRAYGRMQRVASRVIGAII 208
         ||:|   ||:| | |  : |
Db  195 AVVRRGLARAQGVVDKLLGGLL 216
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RESULT 8
US-09-328-352-4775
; Sequence 4775, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4775
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4775

Query Match   19.4%;   Score 220.5; DB 4;   Length 210;
Best Local Similarity   26.7%;   Pred. No. 1.9e-16;
Matches   54; Conservative   39; Mismatches   106; Indels   3; Gaps   1;

```
Qy   16 PLHAVYLTVGLFVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGL  75
        || :: :::|||  :|::  |:::  ::|:  :  ||  | |  || | | |::||  |
Db   10 PLFSIAMALMLGAI---SPGPSFIYVAQNSISKSRKHGLFTALGTGTGAALFGFLAVMGL  66

Qy   76 ATLITQCEEIFSLIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPISAPWYVFFRRGLITD 135
         ::|   : ||  |  ||| ||||:|      : ||:|   |  : :
Db   67 QAVLLAVPSAYLILKIGGGLYLLMLWLAFKIIKHAKEPIAMENDAKSKMTYKQAYRYGLITQ 126

Qy  136 LSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASIIWRVFLSQAFSLPAVRRAYGR 195
        |||   | | |:|: :|  |:|:|  | |  :   | ::  :  |:  :    :
Db  127 LSNPKIAVVLASVFTALLPKEIPNYYVALPLICFMIDAGWYSCVAMLLSSEKPRKMYLK 186

Qy  196 MQRVASRVIGAIIGVFALRLIY 217
        ::|| | ||  :: :| | |:
Db  187 AKTGVDRVAGSIVSVLGLKLIF 208
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RESULT 9
US-09-328-352-8249
; Sequence 8249, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8249
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii

US-09-328-352-8249

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Query Match            19.4%;    Score 220.5; DB 4;   Length 235;
Best Local Similarity  26.0%;    Pred. No. 2.2e-16;
Matches    56;  Conservative   37;  Mismatches   79;  Indels   43;  Gaps    6;

Qy    7 LFMDEITMDPLHAVYLTVGLFVITF-FNPGANLFVVQTSLASGRRAGVLTGLGVALGDA 65
Db   19 IIFKDISMLDLSQI-LAFGLICLAMVLTPGPNMIYLISRSISQGKIAGFISLGGVAVGFV 77

Qy   66 FYSGLGLFGLATLITQCEEIFSLIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPISAPWY 125
Db   78 FYMLCASFGITALVVAVPYAYDTIRIAGAMYILWLAWKALRPNAAPIFNVKDLAVDSPLK 137

Qy  126 VFFRRGLITDLSNPQTVLFFISIF-----------------------SVTLNA------ 155
Db  138 LFL-MGFLTNLLNPKIAIMYLSLLPQFIHPQQGSILAQSIQLGTIQIFVSVSVNALIVFS 196

Qy  156 -------ETPTWARLMAWA-GIVLASIIWRVFL 180
Db  197 AGSIALFLQKKPLWASIQRWVMGTVLAGLAVRILL 231
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RESULT 10
US-09-252-991A-25992
; Sequence 25992, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25992
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25992

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Query Match            18.2%;    Score 207; DB 4;   Length 260;
Best Local Similarity  27.3%;    Pred. No. 7.8e-15;
Matches    57;  Conservative   44;  Mismatches   94;  Indels   14;  Gaps    4;

Qy   12 ITMDPLHAVYLTVGLFVITFFNPGANLFVVQTSLASGRRAGVLTGLGVALGDAFYSGLG 71
Db   46 VAMQELSVLLTLAAVFAIALVSPGDVALVVRTSLHQGRRAGLASALGLACGILLHTTLIV 105

Qy   72 LFGLATLITQCEEIFSLIRIVGGAYLLWFAWCSMR---RQSTPQMSTLQQPIS----APW 124
Db  106 LTGVSLLLSRTPVLFAILQALGALYLAWLGVGALRAWLRRGDCQPGRLDGALPPSPLGPW 165

Qy  125 YVFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASIIWRVFLSQAF 184
Db  166 L-----RGVATNLFNPKALVLFIALLGSLIPAQMSLGGKLAVAALLFGMGACWFGLLSLTL 221

Qy  185 SLPAVRRAYGRMQRVASRVIGAIIGVFAL 213
Db  222 TRPALQ--ARLLRAVPWLDAACGVVFLL 247
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RESULT 11
US-09-489-039A-8849
; Sequence 8849, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8849
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8849

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Query Match            16.8%;    Score 190.5; DB 4;   Length 231;
Best Local Similarity  27.0%;    Pred. No. 4.5e-13;
Matches    60;  Conservative   45;  Mismatches   92;  Indels   25;  Gaps    7;

Qy   11 EITMDPLHAVY------------LTVGLFVITFFNPGANLFVVQTSLASGRRAGVLTGLGVALGD 64
Db    8 EATMHTLSTLFPAVFPALALSHFV-ALLSPGDFFLLIGYAVRYRIRGSIGLCLGIAAGN 66

Qy   65 AFYSGLGLFGLATLITQCEEIFSLIRIVGGAYLLWFAWCSMR-RQSTPQMSTLQQPISAP 123
Db   67 ALYIVLAIVGWG-LLRQAPLFLPLLIELLGAGYLLWIGSLLIRSRPATLAMESVRAARPGF 125

Qy  124 WYVFFRRGLITDLSNPQTVLFFISIF------SVTLNAETPTWARLMAWAGIVLASII-- 175
Db  126 GRQLLLLGLGSSLLNPKNALFYLALMTSLLGPAVTLLQQTV--------SGLWMVSVVFF 177

Qy  176 WRVFLSQAFSLPAVRRAYGRMQRVASRVIGAIIGVFPALRLIY 217
Db  178 WDLLLVSAIALPQIQRRLGAIVWRVERAAGAILMLFGLGIIW 219
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RESULT 12
US-09-543-681A-4854
; Sequence 4854, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4854
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4854

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Query Match            16.7%;    Score 190; DB 4;   Length 228;
Best Local Similarity  29.8%;    Pred. No. 5e-13;
Matches    62;  Conservative   42;  Mismatches   66;  Indels   38;  Gaps   10;

Qy   21 YLTVGLFVITFFNPGANLFVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLATLIT 80
Db   29 YL-AGMFFIIIV-PGPNSLYVLKTSASRGVGAGYRAALGVFIGDAILLIFLAFIGVASVIK 86

Qy   81 QCEEIFSLIRIVGGAYLLW--------FAWCSMRRQSTPQMSTLQQPISAPWYVFFRR 130
Db   87 ASPVLFTIVRFLGAFYLLYLGIKIIIHANFFA----KKQSHTETNCIQEHV------FRK 135

Qy  131 GLITDLSNPQTVLFFISIFSVTLN--AETPTWARLMAWAGIVLASIIWR---VFLS-QA 183
Db  136 AITLSLINPKALFYISFFVQFIDFNYAHT------GLSYILASMLEAFSFVYLSFLI 188

Qy  184 FSLPAVRRAYGRMQRVASRVIGAIIGVF 211
Db  189 FGGVALARFFGSRKNIA-KLGNGIVGLF 215
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RESULT 13
US-09-328-352-4784
; Sequence 4784, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4784
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4784

Query Match   16.4%; Score 186; DB 4; Length 206;
Best Local Similarity   23.5%; Pred. No. 1.2e-12;
Matches   47; Conservative   51; Mismatches   98; Indels   4; Gaps   2;

Qy   19 AVYLTVGLF-VITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLAT 77
          | :::| || ::||: :|| ||: |||:|| ||:|:|||
Db   6 AEFIAVILITILAVVSPGADFAIVTKNSYLYGRKIGVFTSLGISLGVLHVTVTLVAVTF 65

Qy   78 LITQCEEIFSLRIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPISAPWYVFFRRGLITDLS 137
          ||:|| :|| : ||||||||||||| | ::| :| | | |::: |:
Db   66 VMTYTPQILNIVKYIGALYLLYIGYKTFTQKPVLDSAAL---TAIGTFQAIKYGFFTNAL 122

Qy 138 NPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASIIWRVFLSQAFSLPAVRRAYGRMQ 197
          | :|| || ||| ||: |||| |:|| ||| ::| :||
Db 123 NPKTLFVISTYTQIVSLTTPKTVLLAYGFFMSFAHFVWFSLVAMLFSSMLLRQKMLAKQ 182

Qy 198 RVASRVIGAIIGVFALRLIY 217
          ::||:: |: : |::|
Db 183 VQINKVIGSLLCVLGVILLF 202

RESULT 14
US-09-328-352-5111
; Sequence 5111, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5111
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5111

Query Match   16.0%; Score 182; DB 4; Length 208;
Best Local Similarity   27.7%; Pred. No. 3.4e-12;
Matches   46; Conservative   43; Mismatches   63; Indels   14; Gaps   7;

Qy   20 VYLTVGLFVITF-FNPG-ANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLAT 77
          ::: || | || :|| | | ||: | |:: |: |:| |:|
Db   7 LFITFLITTIIFAYIPGPAMLYTAAQT-LSRGRKSGLMAAFGIFVGGCFHIIAASLGLTT 65

Qy   78 LITQCEEIFSLRIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPISAPWYVFFRRGLITDLS 137
          ::: :|:|:||| |||:|| |||:| | : | || :: :: :
Db   66 IFQIIPKLYDIIKILGALYLVWLGIKLIRSTSSP---TLQQNVE-NGQLSLRQSIIVEVL 121

Qy 138 NPQTVLFFISIFSVTLNA--ETPTWARLMAWAGIVLASIIWRVFLS 181
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                GenCore version 5.1.6
        Copyright (c) 1993 - 2005  Compugen Ltd.
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OM protein - protein search, using sw model

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Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	217	19.1	226	9	US-09-738-626-3665	Sequence 3665, Ap
2	179	15.8	207	9	US-09-738-626-6418	Sequence 6418, Ap
3	175	15.4	217	14	US-10-156-761-10918	Sequence 10918, A
4	168	14.8	205	14	US-10-156-761-11297	Sequence 11297, A
5	166	14.6	223	9	US-09-738-626-6070	Sequence 6070, Ap
6	166	14.6	223	17	US-09-746-660A-14	Sequence 14, Appl
7	166	14.6	212	15	US-10-494-672-296	Sequence 296, App
8	162	14.3	206	15	US-10-374-903A-6	Sequence 6, Appli
9	145.5	12.8	209	15	US-10-282-122A-78024	Sequence 78024, A
10	143	12.6	206	15	US-10-282-122A-66814	Sequence 66814, A
11	141.5	12.5	206	15	US-10-282-122A-75782	Sequence 75782, A
12	140.5	12.4	224	14	US-10-156-761-7796	Sequence 7796, Ap
13	138.5	12.2	205	15	US-10-282-122A-76964	Sequence 76964, A
14	138	12.2	205	15	US-10-282-122A-72863	Sequence 72863, A
15	135	11.9	211	15	US-10-282-122A-47826	Sequence 47826, A
16	134	11.8	227	15	US-10-461-194-94	Sequence 94, Appl
17	133	11.7	206	15	US-10-461-194-124	Sequence 124, App
18	132.5	11.7	209	15	US-10-282-122A-56211	Sequence 56211, A
19	127.5	11.2	205	15	US-10-282-122A-51102	Sequence 51102, A
20	126.5	11.1	205	9	US-09-927-395-2	Sequence 2, Appli
21	126.5	11.1	206	9	US-09-847-392-2	Sequence 2, Appli
22	125	11.0	211	15	US-10-282-122A-60157	Sequence 60157, A
23	124.5	11.0	211	15	US-10-282-122A-67883	Sequence 67883, A
24	123.5	10.9	210	15	US-10-282-122A-69338	Sequence 69338, A
25	114	10.0	203	14	US-10-156-761-8659	Sequence 8659, Ap
26	108.5	9.6	210	14	US-10-156-761-14994	Sequence 14994, A
27	108	9.5	227	14	US-10-264-104-5	Sequence 5, Appli
28	100	8.8	181	15	US-10-282-122A-44873	Sequence 44873, A
29	100	8.8	195	15	US-10-620-487-2	Sequence 2, Appli
30	96	8.4	211	15	US-10-282-122A-56075	Sequence 56075, A
31	95	8.2	631	15	US-10-282-122A-43089	Sequence 43089, A
32	93.5	8.2	211	15	US-10-282-122A-69966	Sequence 69966, A
33	93	8.2	211	15	US-10-282-122A-59719	Sequence 59719, A
34	93	8.1	940	15	US-10-282-122A-64286	Sequence 64286, A
35	92	8.1	211	15	US-10-282-122A-73496	Sequence 73496, A
36	92	8.1	211	15	US-10-282-122A-76048	Sequence 76048, A
37	92	8.1	233	10	US-09-746-660A-52	Sequence 52, Appl
38	92	8.1	233	15	US-10-196-232-25	Sequence 25, Appl
39	92	8.1	236	9	US-09-738-626-6955	Sequence 6955, Ap
40	92	8.1	236	14	US-10-166-142-8	Sequence 8, Appli
41	92	8.1	236	16	US-10-716-473-8	Sequence 8, Appli
42	92	8.1	236	17	US-10-760-283-18	Sequence 18, Appl
43	92	8.1	236	17	US-10-784-986-22	Sequence 22, Appl
44	92	8.1	236	17	US-10-716-470-8	Sequence 8, Appli
45	90	7.9	386	15	US-10-282-122A-78364	Sequence 78364, A

ALIGNMENTS

RESULT 1
US-09-738-626-3665
; Sequence 3665, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWA, SATOSHI
;   APPLICANT: MIZOGUCHI, HIROSHI
;   APPLICANT: ANDO, SEIKO
;   APPLICANT: HAYASHI, MIKIRO
;   APPLICANT: OCHIAI, KEIKO
;   APPLICANT: YOKOI, HARUHIKO
;   APPLICANT: TATEISHI, NAOKO
;   APPLICANT: SENOH, AKIHIRO
;   APPLICANT: IKEDA, MASATO
;   APPLICANT: OZAKI, AKIO
;   TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;   FILE REFERENCE: 249-125
;   CURRENT APPLICATION NUMBER: US/09/738,626
;   CURRENT FILING DATE: 2000-12-18
;   PRIOR APPLICATION NUMBER: JP 99/377484
;   PRIOR FILING DATE: 1999-12-16
;   PRIOR APPLICATION NUMBER: JP 00/159162
;   PRIOR FILING DATE: 2000-04-07
;   PRIOR APPLICATION NUMBER: JP 00/280988
;   PRIOR FILING DATE: 2000-08-03
;   NUMBER OF SEQ ID NOS: 7059
;   SOFTWARE: PatentIn ver. 3.0
;   SEQ ID NO 3665
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-3665

Query Match   19.1%;   Score 217; DB 9; Length 226;
Best Local Similarity 28.6%;   Pred. No. 2e-14;
Matches 63; Conservative 48; Mismatches 81; Indels 28; Gaps 7;

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Qy   19 AVLTVGLFVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLATL 78
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Db    8 ALFL---VWIAAIASPGDLFQIIRLS-AKNRRDGVLTAVGIMVGNSIWIIASLLGLSAL 63

Qy   79 ITQCEEIFSLIRIVGGAYLLWFAWCSMR----RQSTPQMSTLQQPI--------SAPW 124
        |:      :||| ||| |                ::||
Db   64 ISTYPAILNLQLVGGGYLTMWGIGAVRSWWTKRSTQQAAADSQAVENTLVTATAASVGV 123

Qy  125 YVFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASIIWRVFLSQAF 184
          | | ||||  :|:||::|| |||  :|:    ||| ||| |||||||||||:||||
Db  124 WPAIRSGIATNLSNPKAVLFFGSVFAQFVRPDMGIGWSIFIGVFLLTGLLWFV----GF 179

Qy  185 SLPAVRRAYGRMQRVASRVIGAIIGVFALRL----IYEGV 220
        :  |: |:|     :|: ||| |||| |||||    |||||
Db  180 AVLVRKLAAGLTRNGA--IIDLLTGVIFIGLGMFMIFEGV 217


RESULT 2
US-09-738-626-6418
; Sequence 6418, Application US2002019760SA1
; Publication No. US2002019760SA1
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWA, SATOSHI
;   APPLICANT: MIZOGUCHI, HIROSHI
;   APPLICANT: ANDO, SEIKO
;   APPLICANT: HAYASHI, MIKIRO
;   APPLICANT: OCHIAI, KEIKO
;   APPLICANT: YOKOI, HARUHIKO
;   APPLICANT: TATEISHI, NAOKO
;   APPLICANT: SENOH, AKIHIRO
;   APPLICANT: IKEDA, MASATO
;   APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6418
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6418

Query Match             15.8%;  Score 179;  DB 9;  Length 207;
Best Local Similarity   31.6%;  Pred. No. 1.8e-10;
Matches   65;  Conservative   32;  Mismatches   87;  Indels   22;  Gaps   9;

Qy   19 AVYLTVGLFVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLATL 78
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Db   10 ALALLVALAV-----PGPDL-VLVLHSATRGIRTGVMTAAGIMTGLMLHASLAIAGATAL 63

Qy   79 ITQCEEIFSLIRIVGGAYLLWFAWCSMR-RQSTPQMSTLQQPISAPWVVFRRGLITDLS 137
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Db   64 LLSAPGVLSAIQLLGAGVLLWMGTNMFRASQNTGESETAASQSSAGYF----RGFITNAT 119

Qy  138 NPQTVLFFISIFSVTL-NAETPTWARLMAWAGIVLASIIWRVFLSQAFSLPAVRRAYGRM 196
        || ||| | ::  |:  |       |:||: | ::|  |  |
Db  120 NPKALLFFAAILPQFIGNGEDMGMRTLALCATIVLGSGAWWL------GTIALVRGIG-L 172

Qy  197 QRV--ASRVIGAIIGVFALRLIYEGV 220
        |::   ||:| |:| |||| | |||
Db  173 QKLPSADRII-TLVGGIALFLIGAGL 197


RESULT 3
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US-10-156-761-10918
; Sequence 10918, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;   APPLICANT: OMURA, SATOSHI
;   APPLICANT: IKEDA, HARUO
;   APPLICANT: ISHIKAWA, JUN
;   APPLICANT: HORIKAWA, HIROSHI
;   APPLICANT: SHIBA, TADAYOSHI
;   APPLICANT: SAKAKI, YOSHIYUKI
;   APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10918
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10918

Query Match             15.4%;  Score 175;  DB 14;  Length 217;
Best Local Similarity   27.9%;  Pred. No. 5.2e-09;
Matches   60;  Conservative   34;  Mismatches   97;  Indels   24;  Gaps   8;

Qy   21 YLTVGLFVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLATLIT 80
        ||  ||:|::||  |  |  |: :| ::| :|| | | |   |  :| |
Db   10 YL-AGLVLIVLL-PGPNSLYVLSVAARKGVRAGYTAAAGVWCGDTVLMTLSAAGVASLLQ 67

Qy   81 QCEEIFSLIRIVGGAYLLWFAWCSMR------RQSTPQMSTLQQPIS----APWYVFPR 129
         | :||  | | |||| ||  |            :|::        |      |  |  |
Db   68 ANALLFGIVKYAGAGYLTWLAFGMLRAAWEMWRTRRDRADAARAPVAPVAGERP----FR 123

Qy  130 RGLITDLSNPQTVLFFISIF--SVTLNAETPTWARLMAWAGIVLASIIWRVFLSQAFSLP 187
        |  :  |:|||  |||:: |      ||  |  ||:  |  |::: :| | |::: :
Db  124 RAFVVSLFNPKAILFFVAFFVQFVDPGYAYPALSFVVLGAFAQLASFLYLTAL--IFSGT 181

Qy  188 AVRRAYGRMQRV--ASRVIGAIIGVFALRLIYEG 219
        ::| :  |::|   |:    | | |   |||
Db  182 KLAAAFRRKRLSAGATTAAGALFLGFAVKLTLAG 216


RESULT 4
US-10-156-761-11297
; Sequence 11297, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;   APPLICANT: OMURA, SATOSHI
;   APPLICANT: IKEDA, HARUO
;   APPLICANT: ISHIKAWA, JUN
;   APPLICANT: HORIKAWA, HIROSHI
;   APPLICANT: SHIBA, TADAYOSHI
;   APPLICANT: SAKAKI, YOSHIYUKI
;   APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 11297
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11297
```

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Query Match           14.8%;   Score 168;   DB 14;   Length 205;
Best Local Similarity 25.9%;   Pred. No. 2.6e-09;
Matches 52;  Conservative 39;  Mismatches 90;  Indels 20;  Gaps  8;

Qy   19 AVLTVGLFVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLATL 78
        |:||:|:|.|:::.||||::|                |.|.:|:|||:||
Db    7 AAFLAIDLLLV--FTPGADWAYAIAAGLRD--RSVVPAVAGLVAGYTLLAVAGLVVI 62

Qy   79 ITQCEBIFSLIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPISAPWYVFFRRGLITDLSN 138
        :: .:||:| |:| | ||:||
Db   63 VAGSASLLTALTVLGAAYLIWLGWSVLARPATPQASA-EAVAASRWIVLRCGAGISGL-N 120

Qy  139 PQTVLFFISIFSVTLN-------AETPTWARL-MAWAGIV--LASIIWRVFLSQAFSLP 187
        | |:|:|:| |::    :: :| |           |:|| |
Db  121 PKALLLYFSLFPQFIHPGEGWPVAAQTGLFGTLHMASCAVVVLAVGVLARTVLK---ARP 177

Qy  188 AVRRAYGRMQRVASRVIGAII 208
        ||:  ||| |
Db  178 TAARAVARVSGTMMVIGGFL 198

RESULT 5
US-09-738-626-6070
; Sequence 6070, Application US/09738626
; Publication No. US2002019760 5A1
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWA, SATOSHI
;   APPLICANT: MIZOGUCHI, HIROSHI
;   APPLICANT: ANDO, SEIKO
;   APPLICANT: HAYASHI, MIKIRO
;   APPLICANT: OCHIAI, KEIKO
;   APPLICANT: YOKOI, HARUHIKO
;   APPLICANT: TATEISHI, NAOKO
;   APPLICANT: SENOH, AKIHIRO
;   APPLICANT: IKEDA, MASATO
;   APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6070
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6070

Query Match           14.6%;   Score 166;   DB 9;   Length 223;
Best Local Similarity 26.0%;   Pred. No. 4.7e-09;
Matches 56;  Conservative 50;  Mismatches 83;  Indels 26;  Gaps  7;

Qy   26 LFVITFFNPGANLFVVVQTSLASGRRAGVLTGL-GVALGDAFYSGLGLFGLATLITQCEE 84
        | ::  | |||.|  :: ||| :: | | |:|| | |::
Db   12 LNLVGSLSPGPDTFFLLR--LATRSRAHAIAGVAGIVTGLTVWVTLTVVGAAALLTTYPS 69

Qy   85 IFSLIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPISA-----PWYV-------FFRRG 131
        | :||||||||| : :| |            ::::| |          :|:| |
Db   70 ILGIIQLVGGTYLSFIGYKLLRSASRELIDARQFRNADARPIPDAVEALGTRTQVYRQG 129

Qy  132 LITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASIIWRVFLSQA-----FSL 186
        |:| |||| .|  : | |.| :|    | :   |:|| |: | :  |:|:  |   |:|
Db  130 LATNLSNPKVVMYFAAILAPLMPAHP---SPVLAFS--IIVAILVQTFVTFSAVCLIVST 184

Qy  187 PAVRRAYGRMQRVASRVIGAIIGVFALRLIYEGVT 221
        |:|:|  | :  ::  | : :|||:|||||:|:|
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```
Db  185 ERVRKAMLRAGPWFDLLAGVVFLVVGVTLLYEGLT 219

RESULT 6
US-09-746-660A-14
; Sequence 14, Application US/09746660A
; Publication No. US20030049804A1
; GENERAL INFORMATION:
;   APPLICANT: Pompejus, Markus
;   APPLICANT: Kroger, Burkhard
;   APPLICANT: Schroder, Hartwig
;   APPLICANT: Zelder, Oskar
;   APPLICANT: Haberhauer, Gregor
;   APPLICANT: Kim, Jun-Won
;   APPLICANT: Lee, Heung-Schick
;   APPLICANT: Hwang, Byung-Joon
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CP2
; CURRENT APPLICATION NUMBER: US/09/746,660A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/606740
; PRIOR APPLICATION FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 09/603124
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 14
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-746-660A-14

Query Match           14.6%;   Score 166;   DB 10;   Length 223;
Best Local Similarity 26.0%;   Pred. No. 4.7e-09;
Matches 56;  Conservative 50;  Mismatches 83;  Indels 26;  Gaps  7;

Qy   26 LFVITFFNPGANLFVVVQTSLASGRRAGVLTGL-GVALGDAFYSGLGLFGLATLITQCEE 84
        | ::  | |||.|  :: ||| :: | | |:|| | |::
Db   12 LNLVGSLSPGPDTFFLLR--LATRSRAHAIAGVAGIVTGLTVWVTLTVVGAAALLTTYPS 69

Qy   85 IFSLIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPISA-----PWYV-------FFRRG 131
        | :||||||||| : :| |            ::::| |          :|:| |
Db   70 ILGIIQLVGGTYLSFIGYKLLRSASRELIDARQFRNADARPIPDAVEALGTRTQVYRQG 129

Qy  132 LITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASIIWRVFLSQA-----FSL 186
        |:| |||| .|  : | |.| :|    | :   |:|| |: | :  |:|:  |   |:|
Db  130 LATNLSNPKVVMYFAAILAPLMPAHP---SPVLAFS--IIVAILVQTFVTFSAVCLIVST 184

Qy  187 PAVRRAYGRMQRVASRVIGAIIGVFALRLIYEGVT 221
        |:|:|  | :  ::  | : :|||:|||||:|:|
Db  185 ERVRKAMLRAGPWFDLLAGVVFLVVGVTLLYEGLT 219

RESULT 7
US-10-494-672-296
; Sequence 296, Application US/10494672
; Publication No. US2005000349A1
; GENERAL INFORMATION:
;   APPLICANT: Zelder, Oskar
;   APPLICANT: Pompejus, Markus
;   APPLICANT: Schroder, Hartwig
;   APPLICANT: Kroger, Burkhard
```

```
; APPLICANT: Klopprogge, Corinna
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: Genes coding for novel proteins
; FILE REFERENCE: BGI-16-9US
; CURRENT APPLICATION NUMBER: US/10/494,672
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: PCT/EP02/12134
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: DE 10154177
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 434
; SEQ ID NO 296
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-494-672-296

  Query Match           14.6%;  Score 166;  DB 17;  Length 223;
  Best Local Similarity  26.0%;  Pred. No. 4.7e-09;
  Matches    56;  Conservative  50;  Mismatches  83;  Indels  26;  Gaps  7;

Qy   26  LFVITFFNPGANLFVVVQTSLASGRRAGVLTGL-GVALGDAFYSGLGLFGLATLITQCEE  84
Db   12  LNLVGSLSPGPDTFFLLR--LATRSRAHAIAGVAGIVTGLTVWVTLTVVGAAALLTTYPS  69

Qy   85  IFSLIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPISA-----PWYV------FFRRG  131
Db   70  ILGIIQLVGGGTYLSPIGYKLLRSASRELIDARQFRFNADARPIPDAVEALGTRTQVYRQG  129

Qy  132  LITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASIIWRVFLSQA-----FSL  186
Db  130  LATNLSNPKVVMYFAAILAPLMPAHP---SPVLAFS--IIVAILVQTFVTFSAVCLIVST  184

Qy  187  PAVRRAYGRMQRVASRVIGAIIGVFALRLIYEGVT  221
Db  185  ERVRKAMLRAGPWFDLLAGVVFLVVGVTLLYEGLT  219


RESULT 8
US-10-374-903A-6
; Sequence 6, Application US/10374903A
; Publication No. US20040038250A1
; GENERAL INFORMATION:
; APPLICANT: University of Oviedo
; APPLICANT: Astur Pharma, S.A.
; TITLE OF INVENTION: The gene cluster for thienamycin biosynthesis,
; TITLE OF INVENTION: genetic manipulation and utility
; FILE REFERENCE: Thienamycin-UO-AP
; CURRENT APPLICATION NUMBER: US/10/374,903A
; CURRENT FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 6
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Streptomyces cattleya
US-10-374-903A-6

  Query Match           14.3%;  Score 162;  DB 15;  Length 212;
  Best Local Similarity  25.3%;  Pred. No. 1.2e-08;
  Matches    58;  Conservative  36;  Mismatches  93;  Indels  42;  Gaps  8;

Qy   14  MDPLHAVYLT-VGLFVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGL  72
Db    1  MEPMLTTALAFLGACVLIAAAPGPSTMLIIRQSLHS-RRAGPLTVLGNETGVLTWGVVAA  59

Qy   73  FGLATLITQCEEIFSLIRIVGGAYLLWFAWCSMR------RQSTPQMSTLQQPISAPWY  125
Db   60  LGLTALLAASRTAYDVMRIGGAVVLVWYGVQTLRAANRGEARPSAADDEAAVVPRSG-WK  118

Qy  126  VFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAGI------VLASIIWRV  178
Db  119  I-YRSGLLNLANPKAAVFAMSFLPQFVPAGAPKLPVITALAAFQALFEVGYYGMYVWFV  177
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Qy  179  FLSQAFSLPAVRRAYGRMQRVASR--------VIGAIIGVFALRLIYE  218
Db  178  -------------GRMKRVISRAGVRRLEQVSGGVLLLGIRMAVE  211


RESULT 9
US-10-282-122A-78024
; Sequence 78024, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78024
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-10-282-122A-78024

  Query Match           12.8%;  Score 145.5;  DB 15;  Length 206;
  Best Local Similarity  23.8%;  Pred. No. 6.2e-07;
  Matches    49;  Conservative  46;  Mismatches  96;  Indels  15;  Gaps  5;

Qy   12  ITMDPLHAVYLTVGLFVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLG  71
Db    1  MTLDWDWLITYLLTT--LILSLSPGSGAINTMSTAISHGTRGVVASIGGLGLQLGLAVHIVLV  57

Qy   72  LFGLATLITQCEEIFSLIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPISAPWYVFFRRG  131
Db   58  GVGLGALVSQSLLAFEILKWLGAAYLIWLGIQQWRAAGSLDLHALAN--SMPRRKLFKRA  115

Qy  132  LITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASIIWRVFLSQAFSLPAVRR  191
Db  116  VFVNLTNPKSIVFLAALFPQFVLPQQPQVAQYLILGS---TSVIVDIIVMIGYATLATRI  172

Qy  192  A----YGRMQRVASRVIGAIIGVFAL  213
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Db   173 ARWIKSPQQMKLLNRIFG---GLFML 195

RESULT 10
US-10-282-122A-66814
; Sequence 66814, Application US/10282122A
; Publication No. US2004029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66814
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66814

Query Match   12.6%; Score 143; DB 15; Length 209;
Best Local Similarity 25.6%; Pred. No. 1.2e-06;
Matches 53; Conservative 39; Mismatches 89; Indels 26; Gaps 9;

Qy   26 LFVITFF---------NPGANLFVVVQTSLASGRRAGVLITGLGVALGDAFYSGLGLFG 74
Db   1 MLVSTWFAFFLACWAISLSPGAGAIASMSCGLQYGFARGYWNALGLQIGLALQIAIVAAG 60

Qy   75 LATLITQCEBIFSLIRIVGGAYLLWFA---WCSMRRQSTPQ-MST-LQQPISAPWYVFFR 129
Db   61 VGALLATSALAFSLIKWPGVAYLVYLLAVRQW-----QAPPQALSTDGERPLGRP-LTLvL 114

Qy 130 RGLITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAG--IVLASIIWRVFLSQAFSLP 187
Db 115 RGFLVNASNPKAVIFMLAVLPQPIDPHQPLLAQYLIMGGTMIVDLIVMAGYTGLAARVL 174

Qy 188 AVRRAYGRMQRVASRVIGAI-IGVFAL 213
Db 175 RVLRS-PRQQKLVNTFASLFVGAAGL 200

RESULT 11
US-10-282-122A-75782
; Sequence 75782, Application US/10282122A
; Publication No. US2004029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75782
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-10-282-122A-75782

Query Match   12.5%; Score 141.5; DB 15; Length 206;
Best Local Similarity 24.2%; Pred. No. 1.6e-06;
Matches 52; Conservative 46; Mismatches 84; Indels 33; Gaps 8;

Qy   12 ITMDPLHAVYLTVGLFVITFFNPGANLFVVVQTSLASGRR------AGVLTGLGVALGDA 65
Db   1 MTFEWWFAYLLITSTLLSL---SPGSGAINTMTTSINHGYRGAAASIAGLQTGLGI----- 52

Qy   66 FYSGLGLFGLATLITQCEIFSLIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPISAPWY 125
Db   53 -HIVLVGVGLGTLFSRSLIAFEILKWAGAAYLIWLGIQQWRAAGAIDLHTLAQTQSRG-- 109

Qy 126 VFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWAR--LMAWAGIVLASIIWRVF-LS 181
Db 110 RLFKRAIFVNLTNPKSIVFLAALFPQFIMPQQPQLAQYLILGVTTIVVDMIVMTGYATLA 169

Qy 182 QAFS--------LPAVRRAYGRMQRVASRVIGAII 208
Db 170 QRIAAWIKGPKQMKALNKAFGSL----FMLVGALL 200

RESULT 12

US-10-156-761-7796
; Sequence 7796, Application US/10156761
; Publication No. US2003011901A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7796
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7796

```
Query Match      12.4%;  Score 140.5;  DB 14;  Length 224;
Best Local Similarity 22.4%;  Pred. No. 2.3e-06;
Matches  46;  Conservative  38;  Mismatches  78;  Indels  43;  Gaps  6;

Qy   24 VGLFVITFFNPGANLFVVVQTSL---ASGRRAGVLTGLGVALGDAFYSGLGLFGLATLIT 80
            ||::   :  ::  |||||
Db    9 LGVVLVAYVVPGPDFLVVVRSATEHPAKGRAA----ALGAQSGLCVHMLAAAVGLSLIAA 64

Qy   81 QCEEIFSLIRIVGGAYLLWP---AWCSMRRQ--------------STPQMSTLQQPI 120
            :|| :||||| |||    :  :    :     .|
Db   65 RSPAVYDAIRLLGAAYLVLVLGVRAVLAARRAAERAAGREAVGGVEDGTDPRTPEEEAPA 124

Qy  121 SAPWYVFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWARLM------------AWAG 168
            ||   |||:|| ||  ||:||  ::  |        ::
Db  125 HGRWNRSGFTQGFLTNVLNPKAALFFLSILPQFVHGGGSTSRQIFFLGTLDIVIGVAYNFA 184

Qy  169 IVLASIIWRVFLSQAFSLPAVRRAY 193
            :|  :|: ::  ||
Db  185 LVAVAARLRAFLAR---PKVRHGW 205
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RESULT 13
US-10-282-122A-76964
; Sequence 76964, Application US/10282122A
; Publication No. US2004029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76964
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-76964

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Query Match      12.2%;  Score 138.5;  DB 15;  Length 205;
Best Local Similarity 22.4%;  Pred. No. 3.4e-06;
Matches  38;  Conservative  41;  Mismatches  76;  Indels  15;  Gaps  4;

Qy    5 VHLFMDEITMDPLHAVVLTVGLFVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGD 64
          :|:|:                 :||  :: |:|| ::|:
Db   .3 IHVWL----------AYLLTAVVFSLA---PGSGTVNSISNGLSYGTRHSLGAIIGLQIGL 50

Qy   65 AFYSGLGLFGLATLITQCEEIFSLIRIVGGAYLLWFAWCSMRRQSTPQMSTLQQPISAPW 124
          |    | || ::|  |:|: :||:|| | | ::
Db   51 ACHIVLVGIGIGALVAQSALAFTLIKWIGAAYLVWLGIQKWRDRAPLTATTISHELSQA- 109

Qy  125 YVFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLASI 174
          :.: :|:|:|||:|||    ::
Db  110 -ALLRKAVLINLTNPKSIVFLVALFPQPIDPTRDHWPQFLV-LGITTVTI 157
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RESULT 14
US-10-282-122A-72863
; Sequence 72863, Application US/10282122A
; Publication No. US2004029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578

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;   PRIOR FILING DATE: 2000-09-09
;   PRIOR APPLICATION NUMBER: 60/242,578
;   PRIOR FILING DATE: 2000-10-23
;   PRIOR APPLICATION NUMBER: 60/253,625
;   PRIOR FILING DATE: 2000-11-27
;   PRIOR APPLICATION NUMBER: 60/257,931
;   PRIOR FILING DATE: 2000-12-22
;   PRIOR APPLICATION NUMBER: 60/267,636
;   PRIOR FILING DATE: 2001-02-09
;   PRIOR APPLICATION NUMBER: 60/269,308
;   PRIOR FILING DATE: 2001-02-16
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 78614
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 47826
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Burkholderia cepacia
US-10-282-122A-47826

Query Match       11.9%;  Score 135; DB 15;  Length 211;
Best Local Similarity   25.1%;  Pred. No. 8.1e-06;
Matches   54;  Conservative  39;  Mismatches  92;  Indels  30;  Gaps  10;

Qy   17 LHAVYLTVGLFVITFFNPGANLFVVVQTSLASGRR------AGVLTGLGVALGDAFYSGL 70
          ||:|| .|||||||:|:|:|      :||||.:||::      :||:||||||:||:||
Db    3 LHTWWLFVATVFVVSAIPGPNMLLVMTHGARHGLRRSSATMAGCLSALVLML------AV 56

Qy   71 GLFGLATLITQCEEIFSLIRIVGGAYLLWF--AWCSMRRQSTP--QMSTLQQPISAPWY 125
          . |||  :|  ::|| |:.|| |:|| :   ||  .:|:|:||||:||:  :
Db   57 SAAGLGAVLEAWPAMFNGLRFAGAAYLIYLGVKAW-RARVDDTPAADVDAVSHGASASRA 115

Qy  126 VFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWARLMAWAGIVLAS----IIW-RVF 179
          | .:||:::  :||:|| :|  |.  |:|  ||||     :| :|||       :|:.|
Db  116 VLFRNGFIVAGSNPKAILFAAALLPQFINAAEPTLPQF----GILVVTFAVIEVSWYLVY 171

Qy  180 LSQAFSLPAVRRAYGRMQRVASRVIGAI-IGVFAL 213
          .|  : :|| :| :|   .:|.   |.|  ||:|
Db  172 ASFGTRIGATLKSQS-VAKVFNRLTGGLFVGFGAM 205
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Search completed: January 25, 2005, 16:49:05
Job time : 147 secs

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;   PRIOR FILING DATE: 2000-10-23
;   PRIOR APPLICATION NUMBER: 60/253,625
;   PRIOR APPLICATION NUMBER: 2000-11-27
;   PRIOR APPLICATION NUMBER: 60/257,931
;   PRIOR FILING DATE: 2000-12-22
;   PRIOR FILING DATE: 2001-02-09
;   PRIOR FILING DATE: 2001-02-16
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 78614
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 72863
;   LENGTH: 205
;   TYPE: PRT
;   ORGANISM: Salmonella paratyphi A
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (169)..(169)
;   OTHER INFORMATION: X=any amino acid
US-10-282-122A-72863

Query Match       12.2%;  Score 138; DB 15;  Length 205;
Best Local Similarity   23.9%;  Pred. No. 3.8e-06;
Matches   52;  Conservative  45;  Mismatches  81;  Indels  40;  Gaps  9;

Qy   12 ITMDPLHAVYLTVGLFVITFFNPGANLFVVVQTSLASGRR------AGVLTGLGVALGDA 65
          :|:.| ||.||  :|:     :||.||   :|.||:|:|        :||||||||:
Db    1 MTFEWWFAYLLTSTLLSL---SPGSGAINTMTTSINHGYRGAAASIAGLQTGLGI----- 52

Qy   66 FYSGLGLFGLATLITQCEEIFSLIRIVGGAYLLWFA---WCSMRRQSTPQMSTLQQPISA 122
          |  | ||  :::  ||||  |  : |   :::|           ::|
Db   53 -HIVLVGVGLGTLFSRSLLAFEILKWAGAAYLIWLGIQQW---RAGAIDLHTLAQTQSR 107

Qy  123 PWYVFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWAR--LMAWAGIVLASIIWRVFL 180
          |:|| ...:|.||:|   ||:  | :...:    |||
Db  108 G--RLFKRAIFVNLITNPKSIVFLAALFPQFIMPQQPLAQYLILGVTTIVVDMIVMTGYA 165

Qy  181 SQAF--------SLPAVRRAYGRMQRVASRVIGAII 208
          .|         : :||:
Db  166 TLAXRTAAWIKGPKQMKALNKAFGSL----FMLVGALL 199
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RESULT 15
US-10-282-122A-47826
;   Sequence 47826, Application US/10282122A
;   Publication No. US20040029129A1
;   GENERAL INFORMATION:
;   APPLICANT: Wang, Liangsu
;   APPLICANT: Zamudio, Carlos
;   APPLICANT: Malone, Cheryl
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Kari
;   APPLICANT: Zyskind, Judith
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John
;   APPLICANT: Carr, Grant
;   APPLICANT: Yamamoto, Robert
;   APPLICANT: Forsyth, R.
;   APPLICANT: Xu, H.
;   TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;   FILE REFERENCE: ELITRA.034A
;   CURRENT APPLICATION NUMBER: US/10/282,122A
;   CURRENT FILING DATE: 2003-02-20
;   PRIOR APPLICATION NUMBER: 60/191,078
;   PRIOR FILING DATE: 2000-03-21
;   PRIOR APPLICATION NUMBER: 60/206,848
;   PRIOR FILING DATE: 2000-05-23
;   PRIOR FILING DATE: 2000-05-26
;   PRIOR APPLICATION NUMBER: 60/207,727
;   PRIOR APPLICATION NUMBER: 60/230,335
;   PRIOR FILING DATE: 2000-09-06
;   PRIOR APPLICATION NUMBER: 60/230,347

Wed Jan 26 08:14:34 2005

us-09-459-573-10.rni

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              GenCore version 5.1.6

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OM protein - nucleic search, using frame_plus_p2n model

Run on:    January 25, 2005, 11:53:53 ; Search time 66 Seconds
                                       (without alignments)
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Title:          US-09-459-573-10
Perfect score:  1135
Sequence:       1 MMQLVHLFMDEITMDPLHAV..........IGAIIGVFALRLIYEGVTQR 223

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      Ygapop  10.0 , Ygapext  0.5
      Fgapop   6.0 , Fgapext  7.0
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Searched:       824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters:      1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=local -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09459573 @CGN_1_1_54 @runat_25012005_115348_28875 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      Issued_Patents_NA:*
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        2: /cgn2_6/ptcdata/1/ina/5B_COMB.seq:*
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        6: /cgn2_6/ptcdata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	270	23.8	654	4	US-09-489-039A-905	Sequence 905, App
2	260	22.9	750	4	US-09-328-352-1687	Sequence 1687, Ap
3	245.5	21.6	810	4	US-09-489-039A-149	Sequence 149, App
4	237.5	20.9	645	4	US-09-328-352-2569	Sequence 2569, Ap
5	226	19.9	651	4	US-09-252-991A-2095	Sequence 2095, Ap
6	225	19.8	1830121	4	US-09-557-884-1	Sequence 1, Appli
7	225	19.8	1830121	4	US-09-643-990A-1	Sequence 1, Appli
8	225	19.8	1830121	4	US-10-329-960-1	Sequence 1, Appli
9	224	19.7	660	4	US-09-489-039A-560	Sequence 560, App
10	221	19.5	681	4	US-09-252-991A-15039	Sequence 15039, A
11	220.5	19.4	633	4	US-09-328-352-649	Sequence 649, App
12	220.5	19.4	708	4	US-09-328-352-4123	Sequence 4123, Ap

13	207	18.2	783	4	US-09-252-991A-9421	Sequence 9421, Ap
14	207	18.2	1596	4	US-09-252-991A-9478	Sequence 9478, Ap
15	207	18.2	1650	4 c	US-09-252-991A-9352	Sequence 9352, Ap
16	190.5	16.8	696	4	US-09-489-039A-1678	Sequence 1678, Ap
17	190	16.7	687	4	US-09-543-681A-682	Sequence 682, App
18	186	16.4	621	4	US-09-328-352-658	Sequence 658, App
19	182	16.0	627	4	US-09-328-352-985	Sequence 985, App
20	179	15.8	633	3	US-09-710-279-707	Sequence 707, App
21	179	15.8	675	3	US-09-134-001C-1771	Sequence 1771, Ap
22	179	15.8	2675	4	US-09-710-279-4387	Sequence 4387, Ap
23	179	15.8	2929	4 c	US-09-710-279-3857	Sequence 3857, Ap
24	176	15.5	714	4	US-09-252-991A-10604	Sequence 10604, A
25	176	15.5	816	4 c	US-09-489-039A-10249	Sequence 10249, A
26	173.5	15.3	636	4	US-09-489-039A-2437	Sequence 2437, Ap
27	167.5	14.8	1521	4 c	US-09-252-991A-7437	Sequence 7437, Ap
28	167.5	14.8	2397	4	US-09-252-991A-7203	Sequence 7203, Ap
29	167	14.7	645	4	US-09-489-039A-2622	Sequence 2622, Ap
30	166.5	14.7	687	4	US-09-252-991A-7266	Sequence 7266, Ap
31	165	14.5	726	4	US-09-328-352-3033	Sequence 3033, Ap
32	164	14.4	669	4	US-09-252-991A-10073	Sequence 10073, A
33	164	14.4	1713	4 c	US-09-252-991A-9760	Sequence 9760, Ap
34	164	14.4	2805	4	US-09-252-991A-10208	Sequence 10208, A
35	162	14.3	269223	4 c	US-09-596-002-41	Sequence 41, Appl
36	156.5	13.8	642	4	US-09-255-991A-376	Sequence 376, App
37	156.5	13.8	1656	4	US-09-252-991A-413	Sequence 413, App
38	150.5	13.3	645	4	US-09-543-681A-800	Sequence 800, App
39	144.5	12.7	753	4	US-09-543-681A-315	Sequence 315, App
40	143	12.6	834	4	US-09-252-991A-6447	Sequence 6447, Ap
41	139	12.2	642	4	US-09-489-039A-4674	Sequence 4674, Ap
42	135.5	11.9	639	4	US-09-543-681A-595	Sequence 595, APP
43	135	11.9	633	4	US-09-328-352-2682	Sequence 2682, Ap
44	133	11.7	930	4 c	US-09-252-991A-6103	Sequence 6103, Ap
45	130.5	11.5	723	4	US-09-328-352-3411	Sequence 3411, Ap

ALIGNMENTS

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RESULT 1
US-09-489-039A-905
; Sequence 905, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 905
;  LENGTH: 654
;  TYPE: DNA
;  ORGANISM: Klebsiella pneumoniae
US-09-489-039A-905

Alignment Scores:
Pred. No.:                 9.9e-25        Length:        654
Score:                     270.00         Matches:       64
Percent Similarity:        51.80%         Conservative:  51
Best Local Similarity:     28.83%         Mismatches:    89
Query Match:               23.79%         Indels:        18
DB:                        4              Gaps:          4

US-09-459-573-10 (1-223) x US-09-489-039A-905  (1-654)

Qy      4 LeuValHisLeuPheMetAspGluIleThrMetAspProLeuHisAlaValTyrLeuThr 23
                :::|||
Db      4 CTCCTTCATTATTTTCCTCGCCGAGTTAACTATGCTGATGCTT-------------TTCCTCACC 54
                            |||              ::|||||||              |||

Qy     24 ValGlyLeu---PheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValVal 42
                |||                 :::|||||           ::: |||
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Db   55 GTGGCGCTGGTGCATATCATTGCGCTGATGAGCCCGGGCCGGACTTTTCTTGTCTCA 114

Qy   43 GlnThrSerLeuAlaSerGlyArgArgArgAlaGlyValLeuThrGlyLeuGlyValAlaLeu 62
        ||||||        :::::::        ||||||
Db  115 CAAACGGCCATCAGCCGCCTCGCGAAGAGAGGCGATGATGGGTGTGCTGGGGATCACCTGC 174

Qy   63 GlyLeuAspAlaPheTyrSerGlyLeuPheGlyLeuAlaThrLeuIleThrGlnPheCys 82
        :::  |||     :::   |||
Db  175 GGCGTCATGGGTCTGGGCGGAGTGGGCGGCGTCGCGCTGCTCGCCGAACCTGATCCTGCCCGTATG 234

Qy   83 GluGluIlePheSerLeuIleArgIleValGlyIleLeuTrpPheAlaTrp 102
        :::
Db  235 GCGTGGCTGCATAACATTATTATGTCGGCGGGCGGGGCCTGATCTCATGCTGGATGGGCTAC 294

Qy  103 CysSerMetArg------------------ArgGlnSerThrProGlnMetSer 114
        :::|||
Db  295 CAGATGCTGCGTGGGCGCGTGGGCGCGAAAAAAGAGGACGGTGGCCTCGGCCGGGAG 354

Qy  115 ThrLeuGlnGlnProIleSerAlaProTrpTyrValPhePheArgArgGlyLeuIleThr 134
        :::  :::||||||
Db  355 CTGGGCCCGCAGCGGACGCAGC------------TTCGTGAAGGGATTGCTGACC 396

Qy  135 AspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePheSerValThrLeuAsn 154
        :::  |||:::||||||
Db  397 AATCTGGCGAATCCGAAAGCGATTATCTTACTTCGGCTCGGTGTTTTCGTTGGTTCCGTGGGT 456

Qy  155 AlaGluThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIleLeuValAlaSerIle 174
        :::       :::||||||
Db  457 GACACGGTCGGCGGCGCGCGGCGCTGGGCCATTTCCTGCTGATTATCGTTGAGACGCTG 516

Qy  175 IleTrpArgValPheLeuSerGlnInAlaPheSerLeuProAlaValAlaArgAlaTyrGly 194
        :::|||        :::|||
Db  517 GCCTCTGTTTATGGTGTTGCCAGCCTGTTCGCCCCGGATGCGCCGGCTATCAG 576

Qy  195 ArgMetGlnAsnArgValAlaSerArgValIleGlyAlaAlaIleIleGlyValPheAlaLeuArg 214
        :::|||
Db  577 CGGATGGCGAAGTGGATCGAGCGTATCGCCGGTACGGTTTGCGGGCTTCGGCATCCAC 636

Qy  215 LeuIleIle 216
        ||||||
Db  637 CTGATT 642
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RESULT 2

US-09-328-352-1687
; Sequence 1687, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1687
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1687

Alignment Scores:

Pred. No.:	2.28e-23		Length:	750
Score:	260.00		Matches:	61
Percent Similarity:	52.68%		Conservative:	47
Best Local Similarity:	29.76%		Mismatches:	85
Query Match:	22.91%		Indels:	12
DB:	4		Gaps:	4

US-09-459-573-10 (1-223) x US-09-328-352-1687 (1-750)

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        :::  |||        :::||||||
Db  130 ATGTTAGTCGCGTTAATTACGTTAGCTTTATTCATTTTGTGCGCGTTATTACTCCAGGGG 189
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Qy   36 AlaAsnLeuPheValValValGlnThrSerLeuAlaSerGlyArgArgArgAlaGlyValLeu 55
        :::  ||||||  :  ::|||||||        ::|||
Db  190 CCTGATTTTTTCTGTCATCAGACAGACCGATCTCGAAGAAGCAATGCTG 249

Qy   56 ThrGlyLeuGlyValAlaLeuGlyLeuAspAlaPheTyrSerGlyLeuPheGlyLeuPheLeu 75
        |||:::        |||:::||||||
Db  250 GTTGTTGCAGGAATAACAGTGGGTGTATGTTTTGGCTTCTTTAGCACTGATGGGCTTA 309

Qy   76 AlaThrLeuIleThrGlnCysGluGluIlePheSerLeuIleArgIleValGlyIleGlyAla 95
        :::        :::|||
Db  310 AATATTATTTTTGAGAAAATGGCTTGGTAAAGCAAGGTTTACTTATTGCCGGCGGTTTA 369

Qy   96 TyrLeuLeuTrpPheAlaTrpCysSerMetArg------------------ArgGlnSerThrPro 111
        :::        :::|||
Db  370 TACCTATGCTGGTTAGGATACCAAATGTTGCGTTCGGCCATTTTCAAAAAATCAGCAGGAA 429

Qy  112 GlnMetSerThrLeuGlnLeuGlnProIleSerAlaProTrpTyrValPhePheArgArgGly 131
        :::  :::||||||        :::|||
Db  430 GAAGTGACAACTGTTGAATTACCG---AAAGCGCCG---TATTTATTTTTTATGAAGGGA 483

Qy  132 LeuIleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePheSerVal 151
        ||||||:::  ||||||        :::|||
Db  484 TTACTCACCAATTTATCGAACCCTAAAGCTGTGATCTATTTTGGTAGTGTATTCTTTTA 543

Qy  152 ThrLeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIleValLeu 171
        :::        :::|||
Db  544 TTTTTAGCAAACCCTCAGCTTGATCAAGTCCATTGGCTGCTTTTTATTATTGTGTCGGTT 603

Qy  172 AlaSerIleIleTrpArgValPheLeuSerGlnInAlaPheSerLeuProAlaValAlaArg 191
        :::        :::|||
Db  604 GAAACAAATTTTATGGTTCTGCTTTGTGACTTTTATTTTTCATTACCGGAGTTTTAGAGCC 663

Qy  192 AlaTyrGlyMetGlnAsnArgValAlaSerArgValIleGlyAlaAlaIleIleGlyValPhe 211
        :::        |||
Db  664 GCTTACCGTAATTTTCAAAATGGATTGATGATTTCAGGTGGTATTTCAGGTATTTTACCGTTTTC 723

Qy  212 AlaLeuArgLeuIle 216
        ||||||
Db  724 GGTATTTTCCTGATT 738
```

RESULT 3

US-09-489-039A-149
; Sequence 149, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 149
; LENGTH: 810
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-149

Alignment Scores:

Pred. No.:	1.78e-21		Length:	810
Score:	245.50		Matches:	63
Percent Similarity:	47.17%		Conservative:	37
Best Local Similarity:	29.72%		Mismatches:	101
Query Match:	21.63%		Indels:	11
DB:	4		Gaps:	3

US-09-459-573-10 (1-223) x US-09-489-039A-149 (1-810)

```
Qy   17 LeuHisAlaValTyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAla 36
        |||        :::  |||        :::::::
```

Db 187 CTATCCAGCCTGATGGCCATTGCCGCCGGTGCTGCGTCGATCATGGGGCGTGATCAGTCCCGGCCCA 246

Qy   37 AsnLeuPheValValGlnThrSerLeuAlaSerGlyArgArgAlaGlyValLeuThr 56
Db 247 AGCTTTATTTTGTCGCGCCAATGCCGTGCGTCGCTCGCTCGGTLeuGlyLeuPheGlyLeuAla 306

Qy   57 GlyLeuGlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAla 76
Db 307 GCCCTCCGGTACCGGCGCCGCCCATTTTCTCCATTATGGCGATGCCGCCTGCAG 366

Qy   77 ThrLeuIleThrGlnCysGluCysGluLeuLeuIleArgIleValGlyGlyAlaTyr 96
Db 367 AAGGTGCTCACCGGCGGTGCCGAGCTGTTTATTGGTTGGAAGGTGGCCGGCGGCTCTAT 426

Qy   97 LeuLeuTrpPheAlaTrpCysSerMetArgArgGlnSerThrPro---GlnMetSerThr 115
Db 427 CTGCTGTGGCTGGGCTATAAAATTTTCGCGGGTCGGCGCAGCCGATGGACTTTCCGCC 486

Qy 116 LeuGlnGlnProIleSerAlaProTrpTyrValPhePheArgArgArgGlyLeuIleThrAsp 135
Db 487 AGCGGGATGGCCGGCACCGCCTCTTGCTGAAGACCTTCCCGCACGGCTGTATACTCAG 546

Qy 136 LeuSerAsnProGlnThrValLeuPhePheIleSerIlePheSerValThrLeuAsnAla 155
Db 547 CTCAGCAATCCCAAAACTGCGCTGGTGTTCGGCCTCAATTTTTACCGCCCCTGCTGCCGGCG 606

Qy 156 GluThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIleVal----------- 170
Db 607 CAGATCCCCACC------------GCCTTCTATTACATCGTGCCGCCTGATGAGCTTT 651

Qy 171 LeuAlaSerIleIleTrpArgValPheLeuSerGlnAlaPheLeuSerLeuProAlaValArg 190
Db 652 CTGATCGACGTCAGCTGGTATTCGCTGGTGGCCGCTGGTCGTTGCGACCACCCGCGG 711

Qy 191 ArgAlaTyrArgMetGlnArgValAlaSerArgValAlaIleIleGlyVal 210
Db 712 CGGGTCTACCTGCGCGGGCTGAAGCGGCGGATCGACATCGCACAGCCGACGCGGTGCTGGGGGCG 771

Qy 211 PheAlaLeuArgLeuIleTyrGluGlyValThrGln 222
Db 772 CTGGGCCCTGCGCGGCTTATCGCCACCTCCCTCACCCGC 807

RESULT 4
US-09-328-352-2569
; Sequence 2569, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2569
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-2569

Alignment Scores:
Pred. No.:
Score: 1.29e-20
Percent Similarity: 237.50
Best Local Similarity: 50.50%
Query Match: 29.50%
DB: 20.93%

Length: 645
Matches: 59
Conservative: 42
Mismatches: 96
Indels: 3
Gaps: 2

US-09-459-573-10 (1-223) x US-09-328-352-2569 (1-645)

Qy   21 TyrLeuThrValGlyLeuProLeuPhe---ValIleThrPhePheAsnProGlyAlaAsnLeuPhe 39
Db   31 TTTTTAACGCTAGCTCTTATTCACTTTATGCGGTGATTTTACCGGACCAGAGATTTTGTG 90

Qy   40 ValValValGlnThrSerLeuAlaSerGlyArgArgArgAlaGlyValLeuThrGlyLeuGly 59
Db   91 ATTACCGTAAGACAAAGTGTACGTTATGGCTATTGGTTGTCTGACTGCAATTGGT 150

Qy   60 ValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIle 79
Db 151 AATTGGTGTCGGAATTTCAGTCCATGTGTTTTATACACTGGTTGGTATTGGCTTTTGATT 210

Qy   80 ThrGlnCysGluGlnCysPheSerLeuIleArgIleValGlyGlyAlaTyrLeuLeuTrp 99
Db 211 CAGCAAAGTGAATGGCTTATGTCACTGATCAGAACAGCCGGGGGCGGCTTACTTAGTGTAT 270

Qy 100 PheAlaTrpCysSerMetArgArgGlnSerThrProGlnMetSerThrLeuGlnGlnPro 119
Db 271 TTAGGATGGCAGTGCTTACGTAGCCAGCCGAATACCAAATATTGAAATTAATGGCCAATTA 330

Qy 120 IleSerAlaProTrpTyrValPhe------PheArgArgArgGlyLeuIleThrAspLeuSer 137
Db 331 GACAGTGACACGCCCAGTTTATTTAAAGCGTTTACAATGGGTTTCTCACTAATGCGTTA 390

Qy 138 AsnProGlnThrValLeuPhePheIleSerIlePheSerValThrLeuAsnAlaGluThr 157
Db 391 AACCCCAAAGCCACCATCTTTTTTTCTGGCAATTTTTACGACGATTGTAAGTACGACCACA 450

Qy 158 ProThrTrpAlaArgLeuMetAlaTrpAlaGlyIleValLeuAlaSerIleIleTrpArg 177
Db 451 CCAATGAAAGTTCAGTTTTTTATGGGGTTTGGATGGTGTGATGTGTCAATGCCATTCGGTTT 510

Qy 178 ValPheLeuSerGlnAlaPheLeuSerLeuProAlaValArgArgAlaTyrArgMetGln 197
Db 511 ATGGTGGTGAGTGTACGTTTGCACAGCCTATCGTACGTAAAAGATTTTGGAGTTTGGG 570

Qy 198 ArgValAlaSerArgValAlaIleIleGlyValAlaIleIleGlyAlaLeuArgLeuIleTyr 217
Db 571 GTTTATTTTGACGAGGGTGATGGGAGTGTTATTAATTGGAATTGCATTGAGATTGATTGG 630

RESULT 5
US-09-252-991A-2095
; Sequence 2095, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2095
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-2095

Alignment Scores:
Pred. No.:
Score: 3.76e-19
Percent Similarity: 226.00
Best Local Similarity: 51.27%
Query Match: 29.44%
DB: 19.91%

Length: 651
Matches: 58
Conservative: 43
Mismatches: 90
Indels: 6
Gaps: 3

US-09-459-573-10 (1-223) x US-09-252-991A-2095 (1-651)

Qy   21 TyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheVal 40
Db   55 TTCCTGACCATC------ACTGTGCTTGCCGGTGATCAGCCCCGGCCGATTTCGCCATG 108

```
Qy   41  ValValGlnThrSerLeuAlaSerGlyArgArgAlaGlyValLeuThrGlyLeuGlyVal  60
             ||| ::: ||||| ||||||||||||| :::||||||| |||||
Db  109  GTCTCGCGCAACAGCCTGCTGTATTCCCGCCGCGCCTGCTCACCGGCCTGGGCATC  168

Qy   61  AlaLeuGlyAspAlaPheTyrSerGlyLeuPheGlyLeuAlaThrLeuIleThr  80
             ::: ||| ||| :::
Db  169  GCGCGGGGGGTAACGGTACATGTCGGCTACAGCATCCTCGGCGTCGGTGCGC  228

Qy   81  GlnCysGluGluIlePheSerLeuIleArgIleValGlyAlaTyrLeuLeuTrpPhe  100
             :::||||||| :::::::: ||||||||||||||||||||
Db  229  GAGTCGCTGGGCCTGTTCACCCGCGTGAAGTCGGCGGCCGCCGCCTACCTGGTGTTCCTC  288

Qy  101  AlaTrpCysSerMet-----ArgArgGlnSerThrProGlnMetSerThrLeuGlnGln  118
             ::: ||| :::
Db  289  GGCCTCGCGCATGCTGCTGCCGGAGAGGAACTCGGTGCGGCGAGGACGGCGGCGGCGCC  348

Qy  119  ProIleSerAlaProTrpTyrValPheArgArgGlyLeuIleThrAspLeuSerAsn  138
             :::||:::||| ::|||||||:
Db  349  GGGGTTTCGTCC-----TGGGCGATGTGCGCAGCGGCCTTCCTGACCAATCGCTCAAT  402

Qy  139  ProGlnThrValLeuPhePheIleSerIlePheSerValThrLeuAsnAlaGluThrPro  158
             |||:|||||| ||||||||:::||
Db  403  CCGAAGACCTGCCTGTTCGTGTTCAGCCTGTTCATGCAGGTGATCGATCCGCATACCGCG  462

Qy  159  ThrTrpTrpAlaArgLeuMetAlaTrpAlaGlyIleValLeuAlaSerIleIleTrpArgVal  178
             ||||||:::||| :::: ::: |||
Db  463  TTGCCGGCGCAACTGGCCTACGGGCCTTCATCGCCGTGGCCTGGCGTTCGGC  522

Qy  179  PheLeuSerGlnAlaPheSerLeuProAlaValArgArgAlaTyrArgValMetGlnArg  198
             :::||||||||| ||||| ::: :::||
Db  523  CTGGTCGCGCCTGCTTTCTCTGAGCCCGGCGGCGGCCGGCGCTCCGTTTCCGCCCGG  582

Qy  199  ValAlaSerArgValIleGlyAlaIleIleGlyValPheAlaLeuArgLeu  215
             ::: ||: |:|:::
Db  583  CGCATCGACCAGTTCCTCGCGCGCCCTGCTCGGTCGCGTTTCGGCCGTCCTGCTG  633
```

```
RESULT 6
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
  GENERAL INFORMATION:
    APPLICANT: Fleischmann et al.
    TITLE OF INVENTION: The Nucleotide sequence of
                        the Haemophilus influenzae Rd Genome, Fragments
                        Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Human Genome Sciences, Inc.
    STREET: 9410 Key West Avenue
    CITY: Rockville
    STATE: MD
    COUNTRY: USA
    ZIP: 20850
COMPUTER READABLE FORM:
    MEDIUM TYPE: 3 1/2 inch diskette
    COMPUTER: Dell Pentium
    OPERATING SYSTEM: MS DOS v6.22
    SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/557,884
    FILING DATE: 25-Apr-2000
    CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/476,102
    FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
    NAME: Michelle S. Marks
    REGISTRATION NUMBER: 41,971
    REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 301-309-8504
    TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
```

```
SEQUENCE CHARACTERISTICS:
    LENGTH: 1830121 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
    SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Alignment Scores:
  Pred. No.:                         Length:      1830121
  Score:             225.00          Matches:          60
  Percent Similarity:  44.78%        Conservative:     43
  Best Local Similarity: 26.09%      Mismatches:       87
  Query Match:         19.82%        Indels:           40
  DB:                    4           Gaps:              4

US-09-459-573-10 (1-223) x US-09-557-884-1 (1-1830121)

Qy    4  LeuValHisLeuPheMetAspGluIleThrMetAspProLeuHisAlaValTyrLeuThr  23
            :::||||||||||
Db 1385069 ATTGTGCATTTATTT--------------------------------------------  1385083

Qy   24  ValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValGln  43
            |||||| ::: :::|| :::
Db 1385084 --GGATTA-------------ATGACGCCAGGGCCTGATTTCTTTTATGTAAGTCGA  1385125

Qy   44  ThrSerLeuAlaSerGlyArgArgAlaLeuCysValLeuThrGlyValValAlaLeuGly  63
            ||||| ||||||
Db 1385126 ATGGCGGCAAGTAACCTCCGTCGTAATACAGTTTGTGGCATTTTAGGCATAACCGCCTTGGC  1385185

Qy   64  AspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuGlyLeuAlaThrLeuIleThrCysGlu  83
            |||| ::: :::
Db 1385186 ATCGCTTTTGGGGAAAGCTTCTATGTTGGGATTGGCGGGTGTTGTTCGTTACCATTCCA  1385245

Qy   84  GluIlePheSerLeuIleArgIleValGlyAlaTyrLeuTrpLeuTrpPheAlaTrpCys  103
            :::||:::||| :|||
Db 1385246 GCATTACATGGCCGTTATTATGTTGCTAGGTGGTGGTTACCTAGCATATCTCGGTTTTTA  1385305

Qy  104  SerMetArgArgGlnSerThrPro------------------------------Gln  112
            ||
Db 1385306 ATGGCTGCGCAGTAAAAATACGCTAAATTGAATCGCACTCTGATACTGAATTTAATCAA  1385365

Qy  113  MetSerThrLeuGlnGlnProIleSerAlaProTrpTyrValPhePheArgArgGlyLeu  132
            :::||:::||||| |||
Db 1385366 CAAACCAACAATCAAAAAGAAATT----------------------TTGAAAGGGCTT  1385401

Qy  133  IleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePheSerValThr  152
            ::: ::: ||
Db 1385402 TTAGTGAATTTATCCAATGCAAAAGTCGTGGTGATTTTTAGTAGCGTGATCGCGTTGTC  1385461

Qy  153  LeuAsnAlaGluThrProThrTrpTrpAlaArgLeuMetAlaTrpAlaGlyIleLeuAla  172
            ||| |||
Db 1385462 TTAGTAAATATCACTGAAAATGTGGCAAATTATTCTTGCTTTTGCAGTGATTGTGGTAGAA  1385521

Qy  173  SerIleIleTrpArgValPheLeuSerGlnAlaPheSerLeuProAlaValArgArgAla  192
            ::: |||
Db 1385522 ACATTTTGTTATTTTATGTGATTTCATTGATTTTTCACGTAATAATTGCCAAGCGTTTA  1385581

Qy  193  TyrGlyArgMetGlnArgValAlaSerArgValIleGlyAlaIleIleGlyValPheAla  212
            ::: :::|||
Db 1385582 TACAGTCAATACAGCCGTTATATTGATAAATGGCAGGTATTGTATTTTTATTTTTTGGT  1385641

Qy  213  LeuArgLeuIleTyrGluGlyValThrGln  222
            ::: ::: ||
Db 1385642 TGTGTGCTTGTTTATAACGGATCAACGAA  1385671
```

```
RESULT 7
US-09-643-990A-1
; Sequence 1, Application US/09643990A
; Patent No. 6528289
  GENERAL INFORMATION:
    APPLICANT: Robert D. Fleischmann
               Mark D. Adams
```

```
                Owen White
                Hamilton O. Smith
                J. Craig Venter
  TITLE OF INVENTION: The Nucleotide sequence of
                the Haemophilus influenzae Rd Genome, Fragments
                Thereof, and Uses Thereof
  NUMBER OF SEQUENCES: 1
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Human Genome Sciences, Inc.
    STREET: 9410 Key West Avenue
    CITY: Rockville,
    STATE: MD
    COUNTRY: USA
    ZIP: 20850
  COMPUTER READABLE FORM:
    MEDIUM TYPE: 3 1/2 inch diskette
    COMPUTER: Dell Pentium
    OPERATING SYSTEM: MS DOS v6.22
    SOFTWARE: ASCII Text
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/643,990A
    FILING DATE: 23-Aug-2000
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/487,429
    FILING DATE: 1995-06-07
    APPLICATION NUMBER: 08/426,787
    FILING DATE: 1995-04-21
  ATTORNEY/AGENT INFORMATION:
    NAME: Kenley K. Hoover
    REGISTRATION NUMBER: 40,302
    REFERENCE/DOCKET NUMBER: PB186P1C1
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 301-610-5790
    TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1830121 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Alignment Scores:
Pred. No.:               1.43e-13              Length:       1830121
Score:                   225.00                Matches:      60
Percent Similarity:      44.78%                Conservative: 43
Best Local Similarity:   26.09%                Mismatches:   87
Query Match:             19.82%                Indels:       40
DB:                      4                     Gaps:         4

US-09-459-573-10 (1-223) x US-09-643-990A-1 (1-1830121)

Qy     4 LeuValHisLeuPheMetAspGluIleThrMetAspProLeuHisAlaValTyrLeuThr 23
           ::||||||||||
Db 1385069 ATTGTGCATTTATTT------------------------------------------- 1385083

Qy    24 ValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValGln 43
           ||||||                                     ::: |||||
Db 1385084 ---GGATTA-----------------ATGACGGCCAGGCCTGATTTCTTTATGTAAGTCGA 1385125

Qy    44 ThrSerLeuAlaSerGlyArgArgAlaGlyValLeuThrGlyLeuGlyValAlaLeuGly 63
           ::: :::::: |||||||                   ::: :::: |||||
Db 1385126 ATGGCCGGCAAGTAACTCTCGTCGTAATACAGTTTGTGGCATTTAGGCATAACGGCTTGGC 1385185

Qy    64 AspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGlu 83
           :::||||||        |::: :::     ||||||||
Db 1385186 ATCGACCTTTTGGGGAATGCTTCTATGTTGGGATTGGCCGTGTTGTTCGTTACCATTCCA 1385245

Qy    84 GluIlePheSerLeuIleArgIleValGlyValGlyAlaTyrLeuLeuTrpPheAlaTrpCys 103
           ::: ||:::::||||| :::|::: :::     :::
Db 1385246 GCATTACATGGCGTTATTATGTTGCTAGGTTGGTAGTTACCTAGCATATCTCGGTTTTTA 1385305
```

```
Qy   104 SerMetArgArgGlnSerThrPro--------------------------------Gln 112
           ::: :::
Db 1385306 ATGGCTCGCAGTAAAAAATACGCTAAATTTGAATCGCACTCTGATACTACTGAATTTAATCAA 1385365

Qy   113 MetSerThrLeuGlnLeuProIleSerAlaProTrpTyrValPhePheArgArgGlyLeu 132
           ::::||:::::::::::::
Db 1385366 CAAACCACAATCAAAAAAGAAATT------------------------TTGAAAGGGCTT 1385401

Qy   133 IleThrAspLeuSerAsnProGlnThrValLeuPheIleSerIlePheSerValThr 152
           ::: :::||||||||||| ::: ::||||||| |||:::: |||:::
Db 1385402 TTAGTGAATTTATCCAATGCAAAAGTCGTGGTATTTTTAGTAGCGTGATGTCGCCTGTC 1385461

Qy   153 LeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIleValLeuAla 172
           ||| :::::::::::|||::::::::|||:::||
Db 1385462 TTAGTAAATATCACTGAAATGTGCAAATTATCTTGGCTTTTGCAGTGATTGGTGGTAGAA 1385521

Qy   173 SerIleIleTrpArgValPheLeuSerGlnAlaPheLeuSerLeuProAlaValArgArgAla 192
           |||:::                   ::||||||
Db 1385522 ACATTTCTTATTTTATGTGATTTCATTGATTTTTCACGTAATATTGCCAAGCGTTTA 1385581

Qy   193 TyrGlyArgMetGlnArgValAlaSerArgValIleGlyValIleIleIleGlyValPheAla 212
           |||:::           :::           :::
Db 1385582 TACAGTCAATACAGCCGTTATATTGATAATATGGCAGGTATTGTATTTTTATTTTTGGT 1385641

Qy   213 LeuArgLeuIleTyrGluGluValThrGln 222
           ||| |::::|||:::::
Db 1385642 TGTGTGCTTGTTTATAACGGCATCAACGAA 1385671

RESULT 8
US-10-329-960-1
; Sequence 1, Application US/10329960
; Patent No. 6742927
; GENERAL INFORMATION:
;  APPLICANT: Fleischmann et al.
;  TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fra·
; Patent No. 6742927
;  FILE REFERENCE: PB186P1
;  CURRENT APPLICATION NUMBER: US/10/329,960
;  CURRENT FILING DATE: 2003-01-02
;  PRIOR APPLICATION NUMBER: US 09/643,990
;  PRIOR FILING DATE: 2000-08-23
;  PRIOR APPLICATION NUMBER: US 08/487,429
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: US 08/426,787
;  PRIOR FILING DATE: 1995-04-21
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;  LENGTH: 1830121
;  TYPE: DNA
;  ORGANISM: Haemophilus influenzae
;  FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (4747)..(4747)
;    OTHER INFORMATION: n equals a, t, g or c
;  FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (9921)..(9921)
;    OTHER INFORMATION: n equals a, t, g or c
;  FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (10150)..(10150)
;    OTHER INFORMATION: n equals a, t, g or c
;  FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (29298)..(29298)
;    OTHER INFORMATION: n equals a, t, g or c
;  FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (36543)..(36543)
;    OTHER INFORMATION: n equals a, t, g or c
```

FEATURE:
NAME/KEY: misc_feature
LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (44416)..(44416)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (51602)..(51602)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (100091)..(100091)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:

FEATURE:
NAME/KEY: misc_feature
LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (131360)..(131360)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature

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;  LOCATION: (147197)..(147197)
;  OTHER INFORMATION: n equals a, t, g or c
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (150841)..(150841)
;  OTHER INFORMATION: n equals a, t, g or c
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (152500)..(152500)
;  OTHER INFORMATION: n equals a, t, g or c
;  FEATURE:
;  NAME/KEY: misc_feature
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Alignment Scores:
Pred. No.:   1.43e-13
Score: 225.00
Percent Similarity: 44.78%
Best Local Similarity: 26.09%
Query Match: 19.82%
DB: 4

```
; Sequence 560, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 560
;   LENGTH: 660
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-560
```

Alignment Scores:
Pred. No.:   6.9e-19   Length: 660
Score: 224.00   Matches: 67
Percent Similarity: 50.00%   Conservative: 36
Best Local Similarity: 32.52%   Mismatches: 88
Query Match: 19.74%   Indels: 16
DB: 4   Gaps: 6

US-09-459-573-10 (1-223) x US-09-489-039A-560 (1-660)

```
Qy    18  HisAlaValTyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsn  37
              :::  ||||||  :::||||||:||||||:||||
Db    49  TATTTAACCTATCTGGTCGGGGCGGTGTTTATCATCCTCGTT-----CCTGCCCTAAT 102

Qy    38  LeuPheValValValGlnThrSerLeuAlaSerGlyArgArgAlaGlyValAlaLeuThrGly  57
              ||||||||||||:::::||||||||     ||:||
Db   103  ACGTTTTCGTGCTGAAAACGGGTATTGCCCACGGGTGAAGAAAGGCTATCTGGCGCGG 162

Qy    58  LeuGlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThr  77
              ||||||  ||||||     :::||||
Db   163  GCGGGCGTCTTTATTGGCGACGCAGTGCGTGATGTTTCTGCCTTCGCCGGGTGGCCACG 222

Qy    78  LeuIleThrGlnCysGluGluIlePheSerLeuLleArgIleValGlyGlyValTyrLeu  97
              :::       |||  ||:||      ||:||
Db   223  CTGATTAAAACCACGCCAGTGTTGTTAACGTCGTGGCTATCTCGGGGCAATTTACCTG 282

Qy    98  LeuTrpPheAla--------TrpCysSerMetArgArgGlnSerThrProGlnMetSer 114
              ||||                 :::::
Db   283  CTGTGGCTCGGGGCAAAATGCTCTATGCGGTGCTGACCCAGCGCGACGGCGACCAGTCCGAC 342

Qy   115  ThrLeuGlnGlnProIleSerAlaProTrpTyrValPhePheArgGlyLeuIleThr 134
              :::||||                ||:||
Db   343  GCCAGGCGCGGAGCCGCGGCGAGCGCG-------ATCCTCAAGCGCTCCCTGACCCTG 390

Qy   135  AspLeuSerAsnProGlnThrValLeuPheHeSerIlePhe-----SerValThr 152
              :::::||||||    ::::::                      ||
Db   391  AGCCTGACCAATCCGAAAGCCGATTCGTTTTCATATGTCGTTTTTCGTGCAGTTTATCGAT 450

Qy   153  LeuAsnAlaGluThr-ProThrTrpAlaArgLeuMetAlaTrp-----AlaGlyIleVa 170
              :::||||||      ::::||||        :::||||
Db   451  GTCAACGCCAAAACCCCGGCGTGG---CGTTCTTTATCCTGGCGTGACCCTCGAGGTG 507

Qy   170  lLeuAlaSerIleIleIlePheSerLeuSerGlnAlaPheLeuSerGlnProAlaValAr 190
              |||||         :::||
Db   508  ATTAGCTTCTGCTATATGAGCTTTTGATCCTCTCCGGCTCGTTTGTCACCCGCTACGTC 567

Qy   190  gArgAlaTyrGlyArgMetGlnArgValAlaSerArgValIleGlyAlaIleIleGlyVa 210
              :::::          ||||||  :::||||
Db   568  -AAAACCCGCAAGAGCTGGCTAAACTGGCAACAGCCTGATTGGTCTGGTTTCGTCGG 626

Qy   210  lPheAlaLeuArgLeu 215
              ||||||
Db   627  GTTCGGCGCCGGCCTG 642
```

RESULT 10

US-09-459-573-10 (1-223) x US-10-329-960-1 (1-1830121)

```
Qy     4  LeuValHisLeuPheMetAspGluIleThrMetAspProLeuHisAlaValTyrLeuThr  23
              ::||||||||||||||||||
Db 1385069 ATTGTGCATTTATTT----------------------------------------- 1385083

Qy    24  ValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValGln  43
              ||||                    :::   ||      ||:||
Db 1385084 ---GGATTA-----------------ATGACGCCAGGGCCTGAATTCTTTTATGTAAGTCGA 1385125

Qy    44  ThrSerLeuAlaSerGlyArgArgAlaGlyValAlaLeuThrGlyLeuGlyValAlaLeuGly  63
              :::  :::||||      |||   ||||
Db 1385126 ATGGCGGCAGTAACTCTCGTCGTATACAGTTGTGCGCATTTTAGGCATAACGCCTTGGC 1385185

Qy    64  AspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGlu  83
              ||||||  :::        |||
Db 1385186 ATCGCCTTTGGGGAATGCTTTCTATGTGGGATTGGCGGTGTTCGTTACCCATTCCA 1385245

Qy    84  GluIlePheSerLeuLleArgIleValGlyGlyValTyrLeuLeuTrpPheAlaTrpCys 103
              :::        |||    :::
Db 1385246 GCATTACATGGCGTTATTATGTGCTAGGTGGTAGTTACCTAGCATATCTCGGTTTTTTA 1385305

Qy   104  SerMetArgArgGlnSerThrPro--------------------------Gln 112
              ||| :::
Db 1385306 ATGGCTGCAGTAAAAATACGCTAAATTTGAATCGCACTCTGATACTGAATTTAATCAA 1385365

Qy   113  MetSerThrLeuGlnGlnProIleSerAlaProTrpTyrValPhePheArgGlyLeu 132
              :::::||||||              |||
Db 1385366 CAAACCACAATCAAAAAGAAATT--------------------TTGAAAGGGCTT 1385401

Qy   133  IleThrAspLeuSerAsnProGlnThrValLeuPheHeSerIlePheSerValThr 152
              ||||||       :::||
Db 1385402 TTAGTGAATTTATCCAATGCAAAAGTCGTGGTGTATTTTAGTAGCGGTGATGTCGCCTTGTC 1385461

Qy   153  LeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIleValLeuAla 172
              :::||||
Db 1385462 TTAGTAAATATCACTGAAATGTGGCAAATTATCTTGGCTTTTGCAGTGATTGTGTAGAA 1385521

Qy   173  SerIleIleIlePheSerLeuSerGlnAlaPheLeuSerGlnProAlaValArgArgAla 192
              :::::                     :::||
Db 1385522 ACATTTGTTATTTTGTATTTTATGTCATTGATTTTTCACGTAATATTGCCAAGCGTTTA 1385581

Qy   193  TyrGlyArgMetGlnArgValAlaSerArgValIleGlyAlaIleIleGlyValPheAla 212
              :::           |||
Db 1385582 TACAGTCAAATACAGCCGTTATATTGATAATATGGCAGGTATTGTATTTTTTATTTTTTTGGT 1385641

Qy   213  LeuArgLeuIleTyrGluGlyValThrGln 222
              ||||||:::    :::::
Db 1385642 TGTGTGCTTGTTGTTATAACGGCATCAACGAA 1385671
```

RESULT 9
US-09-489-039A-560

US-09-252-991A-15039
; Sequence 15039, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15039
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15039

Alignment Scores:
Pred. No.:
Score: 1.74e-18   Length: 681
Percent Similarity: 221.00   Matches: 55
Best Local Similarity: 50.00%   Conservative: 46
Query Match: 27.23%   Mismatches: 85
DB: 19.47%   Indels: 16
                                            Gaps: 6

US-09-459-573-10 (1-223) x US-09-252-991A-15039 (1-681)

Qy   18 HisAlaValTyrLeuThrValGlyLeuPheValIleThr----------PhePhe   32
          ::: ||| ::: :|| ::: |||
Db   58 TATCGAATCATGCTGGAAACCTGCTCTTCGTAGCCACCCTGCCACCCTGGGCATGCTC 117

Qy   33 AsnProGlyAlaAsnLeuPheValValGlnThrSerLeuAlaSerGlyArgArgAla   52
          :::|||||| ::: |||:::::::   :::   :::
Db   118 TCGCCCGGCGCCCGGACTTCTTCCTGATCATCCGCAACGCGGCGCCTACCAGCGCTCGGCG 177

Qy   53 GlyValLeuThrGlyLeuGlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeu   72
          ||| ||| ||| ||| ::: ::: :::
Db   178 GGCGATGATGACCTCGCTGGGGGTGATTCTCGGCGTGGCCACCCATGGCCTACTGGCGTC 237

Qy   73 PheGlyLeuAlaThrLeuThrCysGluGlnIleLeuPheSerLeuIleArgIleVal   92
          |||||| ::: |||:::   :::|||||| ::: :::
Db   238 GCCGGCCTGGCGGTGCTGATCACCCACGCCGTGGCTGTTCAACGCGCTGAAGTACACC 297

Qy   93 GlyGlyAlaTyrLeuLeuTrpPheAlaTrpCysSerMetArgArgGlnSerThrProGln 112
          |||||| ||| ::: |||:::   :::
Db   298 GGCGGGGTCTACCTGATCTGGACGAGCATCGGACGGCGTCGCGTCGGCGGCGGCGGC 351

Qy   113 MetSerThrLeuGlnGlnProIleSer--------------AlaProTrpTyrValPhe 127
          ||||||
Db   352 ---GGCACGCTCGACCTGGCGGTCGGCGGCGTCGGGCGCGTCCAGCGCGCCCACTGGACGCCGGTT 408

Qy   128 PheArgArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSer 147
          ||| ::: ::: ||||||| :::::::::::
Db   409 CTC---CAGGGCTACCTGTGCAACCTGCTCAACCCCAAGGCCACACGCTGTTCTTCCTCGCC 465

Qy   148 IlePheSerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpPro 167
          ||||||| :::   ::: :::   :::   ::: ::|||
Db   466 GTGTTCACCCAGGTGCTGAGCCTGGACTCC---AGCTTCGCCGAGAGGCTCTGGTACGCC 522

Qy   168 GlyIleValLeuAla---SerIleIleTrpArgValPheLeuSerGlnInAlaPheSerLeu 186
          ||||| :::   :::   :::
Db   523 GGCATCATCGTCCGCCTCGGTGGCCGCACTCTGGTGGCCGCTCGTGCTGGTGCTGATCCAGAGC 582

Qy   187 ProAlaValArgArgAlaTyrArgMetGlnArgValAlaSerArgValIleGlyValAla 206
          ||| ||| ||| :::||| :::||||||::|||
Db   583 GCGGTGGTGCGCCGCGGCCTGGCCCAGGGCGTGGTGACAAGCTGCTCCGCGCGGC 642

Qy   207 IleIle 208
          ::|||:
Db   643 CTGCTG 648

Db   643 CTGCTG 648

RESULT 11
US-09-328-352-649
; Sequence 649, Application US/0928352
; Patent No. 6552958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 649
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-649

Alignment Scores:
Pred. No.:
Score: 1.8e-18   Length: 633
Percent Similarity: 220.50   Matches: 54
Best Local Similarity: 46.04%   Conservative: 39
Query Match: 26.73%   Mismatches: 106
DB: 19.43%   Indels: 3
                                            Gaps: 1

US-09-459-573-10 (1-223) x US-09-328-352-649 (1-633)

Qy   16 ProLeuHisAlaValTyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGly   35
          |||||| :::   ::: ::: ||| |||
Db   28 CCTCTTTTTCAATTGCGATGGCATTGGAGCAATA----------AGTCCTGGG   78

Qy   36 AlaAsnLeuPheValValGlnThrSerLeuAlaSerGlyArgArgAlaGlyValLeu   55
          ||| :::   :::   ::::: :::
Db   79 CCAAGCTTTATTTGTGTAGCGCAAAATTCAATATCTAAATCACGTAAACATGCTTATTT 138

Qy   56 ThrGlyLeuGlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeu   75
          ::: ||| ||| ::: :::   :::
Db   139 ACGGCTTTAGGAACGGGCACAGTGCAGCTCTTTTTGGCTTTTAGCGGTTATGGGGTTA 198

Qy   76 AlaThrLeuIleThrCysGluGlnIleLeuPheSerLeuIleArgIleGlyGlyAla   95
          :::   ::: ::: ::: |||
Db   199 CAGGCAGTTTTATTGCGAGTGCCTTCAGCTTATCTAATTTTAAAAATTGGTGGTGGGCTG 258

Qy   96 TyrLeuLeuTrpPheAlaTrpCysSerMetArgArgGlnSerThrProGlnMetSerThr 115
          :::   :::
Db   259 TATTTGCTTTGGCTTGCTTTAAAATTATTAAACATGCCAAAGAACCAATTGCTATGGAA 318

Qy   116 LeuGlnGlnProIleSerAlaProTrpTyrValPhePheArgArgGlyLeuIleThrAsp 135
          ::: ||| :::|||||| :::
Db   319 AATGATGCCAAATCGAAGATGACTTATAAACAAGCCTACCGATATGTGTTGATTACTCAG 378

Qy   136 LeuSerAsnProGlnThrValLeuPhePheIleSerIlePheSerValThrLeuAsnAla 155
          ::: ||| :::|||||| :::
Db   379 TTAAGTAATCCAAAAATTGCTGTTGTACTAGCGAGTGTTTTTACTGCTTACTGCCAAAA 438

Qy   156 GluThrProThrTrpAlaArgLeuMetAlaTrpProAlaGlyIleValLeuAlaSerIleIle 175
          ||| ::: :::   :::
Db   439 GAAATTCCAAATTATTACTACGTCGCCATTACCGGCTCATTTGTTTATGATTGATGCAGGT 498

Qy   176 TrpArgValPheLeuSerGlnInAlaPheSerLeuProAlaValArgArgAlaTyrArgArg 195
          |||||:
Db   499 TGGTACTCATGTAGCAAATGCTTTTATCTTCAGAGAAGCCTCGAAAAATGTATTTAAAA 558

Qy   196 MetGlnArgValAlaSerArgValIleGlyValAlaIleIleGlyValPheAlaLeuArgLeu 215
          ||| :::   :::   :::
Db   559 GCAAAAACGGGTGTTGACCGAGTGGTGGAAGCATTGTTAGTATTGGGCTTAAAGTTA 618

Qy   216 IleTyr 217
          ::|||:
Db   619 ATCTTC 624

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us-09-459-573-10.rni

RESULT 12
US-09-328-352-4123
; Sequence 4123, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4123
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4123

Alignment Scores:
Pred. No.:
Score: 2.14e-18
Percent Similarity: 220.50
Best Local Similarity: 43.26%
Query Match: 26.05%
DB: 19.43%

Length: 708
Matches: 56
Conservative: 37
Mismatches: 79
Indels: 43
Gaps: 6

US-09-459-573-10 (1-223) x US-09-328-352-4123 (1-708)

```
Qy    7 LeuPheMetAspGluIleThrMetAspProLeuHisAlaValTyrLeuThrValGlyLeu 26
          :::         ::|||::||  |||   :::   |||   ---TTGGCATTGGATTA 111
Db   55 ATAATATTTAAGGATATATTTCCATGCTAGATCTCTCCAAATT

Qy   27 PheValIleThrPhe---PheAsnProGlyAlaAsnLeuPheValValValGlnThrSer 45
                               |||||          :::   :::
Db  112 ATTTGTCTGGCGATGGTACTCACCCCTGGCCCAAACATGATTTATCTTATCTCCGTTCC 171

Qy   46 LeuAlaSerGlyArgArgAlaGlyValLeuThrGlyLeuGlyValAlaLeuGlyAspAla 65
          :::        |||  |||
Db  172 ATTAGTCAGGGCAAAATCGCAGGATTTATTTCTCCGGTGGCGTTGCCGTTGGTTTTGTA 231

Qy   66 PheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGluGluIle 85
          |||||||                  :::  :::
Db  232 TTTTTACATGCTTTCGCCATCTTCGGGATTACAGCACTTGTTGTTGCAGTACCTTATCCA 291

Qy   86 PheSerLeuLeuIleArgIleValGlyValAlaTyrLeuLeuTrpPheAlaTrpCysSerMet 105
          :::         |||||||||||        |||||||  :::::
Db  292 TATGACACTATTCGTATTGCCGGTGCGATGTACTTACTTGGTTAGCATGGAAAGCTTTA 351

Qy  106 ArgArgGlnSerThrProGlnMetSerThrLeuGlnLeuGlnAsnProIleSerAlaProTrpTyr 125
          ::|||            |||  :::   :::
Db  352 CGCCCCAATGCCGCACCTATTTTAATGTTAAAGATTTAGCCGTTGACTCACCATTAAAG 411

Qy  126 ValPhePheArgArgGlyValGlyLeuIleThrAspLeuSerAsnProGlnThrValLeuPhePhe 145
          ::|||                |||  :::||||||:
Db  412 TTATTTTA--ATGGGCTTTTTGACTAATTTACTTAATTCCTAAAATTGCGATTATGTAT 468

Qy  146 IleSerIlePhe----------------------------------------------------- 149
          ::|||:::
Db  469 TTATCTTTATTACCTCAGTTTATTCACCCACAACAAGGCAGTATTTTAGCGCAGTCTATC 528

Qy  150 ----------------------------------------SerValThrLeuAsnAla 155
                                                  :::
Db  529 CAACTCGGGACTATACAAATTTTTGTAAGCGTTTCAGTAAATGCGCTGATTGTATTTTCT 588

Qy  156 ----------------------GluThrProThrProAlaArgLeuMetAlaTrp 166
                                 :::        :::
Db  589 GCTGGTAGCACAGTATTGCTCTTTTTTCTACAGAAAAAACCACTTTGGGCCAGCATTCAACGCTGG 648

Qy  167 Ala--GlyIleValLeuAlaSerIleIleIleTrpPheArgValPheLeu 180
          |||         |||           |||:
Db  649 GTTCATGGGAACAGTATTAGCCCGGTTCTGCGGTTCGTATTCTTCTA 693
```

RESULT 13
US-09-252-991A-9421
; Sequence 9421, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9421
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9421

Alignment Scores:
Pred. No.:
Score: 1.3e-16
Percent Similarity: 207.00
Best Local Similarity: 48.57%
Query Match: 27.62%
DB: 18.24%

Length: 783
Matches: 58
Conservative: 44
Mismatches: 92
Indels: 16
Gaps: 5

US-09-459-573-10 (1-223) x US-09-252-991A-9421 (1-783)

```
Qy   12 IleThrMetAspProLeuHisAlaValTyrLeuThrValGlyLeuPheValIleThrPhe 31
          :::       |||  :::|||||               :::||
Db  136 GTGACCATGCAGGAATTGTCTGTCTTGCTGACCCTGGCGGCGGTGTTCGCCATAGCCCTG 195

Qy   32 PheAsnProGlyAlaAsnLeuPheValValValGlnThrSerLeuAlaSerGlyArgArg 51
          |||                  :::|||||        ||||||
Db  196 GTCCAGACCCCGTCCGATGTCGCCCTGGTGGTCGCACGTCCTGCACCAGGGGCGGCGGG 255

Qy   52 AlaGlyValLeuThrGlyLeuGlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGly 71
          ||||||      :::        :::||        :::::  |||
Db  256 GCCGGCCTGGCCACGCGCGTGGGCGTGGCCTGCGGAGTTCTCCTGCATACCACCCTGGTG 315

Qy   72 LeuPheGlyLeuAlaThrLeuIleThrGlnCysGluGluIlePheSerLeuLeuIleArgIle 91
          |||  |||          |||:::       :::||::::::
Db  316 CTGACCGGCGTGTCGCGTGCTCAGCCGTACCCTGGTGTTCGCCATCCTGCAGGCG 375

Qy   92 ValGlyValAlaTyrLeuLeuTrpPheAlaTrpCysSerMetArg------ArgGln 108
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Qy  109 SerThrProGlnMetSerThrLeuGln------------------------GlnProIleSerAlaPro 123
          :::||||||        |||  |:::::||
Db  436 GGCGACGGCCAGCCGGCCGGCTCGACGGGCCACTGCCGCCGTCGCCCCTG---GGGCCC 492

Qy  124 TrpTyrValPhePheArgArgGlyValGlyLeuIleThrAspLeuSerAsnProGlnThrValLeu 143
          |||:::         |||:   :::|||  :::        |||||
Db  493 TGGCTG--------------CGCCGAGTGGCGGACCAATCTGTTCAATCCCAAGGCGCTGGTG 540

Qy  144 PhePheIleSerIlePheSerValThrLeuAsnAlaGluThrProThrProAlaArgLeu 163
          ||||||    |||:::             :::|||::||
Db  541 TTATTCATCGCCTTCGTCCGGCAGCCTGATTCCCGCAGATGTCGCTCGGCGGCCAAACTG 600

Qy  164 MetAlaTrpAlaGlyIleValLeuAlaSerIleIleIleTrpPheArgValPheLeuSerGlnAla 183
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Db  601 GCGGTGGCCGGCGCCGCTGCTCGTTCGGCCATGGGCGCCCTGCTGGTTCGGCGGTCGTGGTTGCTGCCTGACC 660

Qy  184 PheSerLeuProAlaValArgArgAlaTyrGlyArgMetGlnArgValAlaSerArgVal 203
          |||||||:::::::         |||
Db  661 CTTACCCGCCGCGGCCCTGCAG-------GCCCGCCTGTTGCGCGGCGTGCCCGTGGGCTG 711

Qy  204 IleGlyAlaIleIleGlyValPheAlaLeu 213
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Db  649 GTTCATGGGAACAGTATTAGCCCGGTTCTGCGGTTCGTATTCTTCTA 693
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Left column (RESULT 14)

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Db   712 GACGCGGCCTGCGGGGTGGTGTTCCTGCTG 741
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RESULT 14
US-09-252-991A-9478
; Sequence 9478, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
;   SEQ ID NO 9478
;   LENGTH: 1596
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9478

Alignment Scores:
Pred. No.:   4e-16   Length: 1596
Score: 207.00   Matches: 58
Percent Similarity: 48.57%   Conservative: 44
Best Local Similarity: 27.62%   Mismatches: 92
Query Match: 18.24%   Indels: 16
DB: Gaps: 5

US-09-459-573-10 (1-223) x US-09-252-991A-9478 (1-1596)

Qy   12 IleThrMetAspProLeuHisAlaValTyrLeuThrValGlyLeuPheValIleThrPhe 31
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Db   35 GTAGCCATGCAGGAGGAATTGTCTGCTGCTGACCGTGGCGCGGTGTTCGCCATAGCCCTG 94

Qy   32 PheAsnProGlyAlaAsnLeuPheValValGlnThrSerLeuAlaSerGlyLysArgArg 51
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Db   95 GTCAGCCCGGTCCCGATGTCGCCCTGGTGGTGCACGGTCCCCTGCACCAGGGCGGCGGG 154

Qy   52 AlaGlyValLeuThrGlyLeuGlyValAlaAlaLeuGlyValAspAlaPheTyrSerGlyLeuGly 71
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Db 155 GCCGGCCTGGCCAGCGGCGTGGGGCTGGCCTGCGCGGGATTCTCTGCATACCACCCTGGTG 214

Qy   72 LeuPheGlyLeuAlaThrLeuIleThrGlnCysGluGluIlePheSerLeuIleArgIle 91
           ||| :::|||:::::::|||
Db 215 CTGACCGGCGGTGCTGCTGCGTGCTGCCAGCGCGGCTCGGGATTCCGCCATCCTGCAGGCG 274

Qy   92 ValGlyGlyAlaTyrLeuLeuTrpPheAlaTrpCysSerMetArg---------ArgGln 108
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Qy 109 SerThrProGlnMetSerThrLeuGln----------GlnProIleSerAlaPro 123
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Db 335 GGCGACGGCCAGCCGGCCGGCCACTGCCGGCGCCCG---GGGCCC 391

Qy 124 TrpTyrValPhePheArgArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeu 143
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Db 392 TGGCTG----------CGCGGAGTGGCGACCAATCTGTTCAATCCCAAGGCGCTGGTG 439

Qy 144 PhePheSerIlePheSerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeu 163
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Db 440 TTATTCATCGCCTTGCTCGGCAGCCTGATGTCGCTCGGCGGCCAAACTG 499

Qy 164 MetAlaTrpAlaGlyIleIleValLeuAlaSerIleIleValPheGlyValPheGlnAla 183
             ||| :::|||
Db 500 GCGGTGGCGGCGCTGCTGTTCGGCATGGGCGCCTGCCTGGTTCGGCCTGACC 559

Qy 184 PheSerLeuProAlaValArgArgAlaTyrArgGlnMetGlnArgValAlaSerArgVal 203
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Db ...
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## Right column (RESULT 15)

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Db   560 CTTACCCGCCCGGCCCTGCAG--------GCCCGCTGTGCGCGGTGCCCTGGCTG 610
              |||                     ||||
Qy   204 IleGlyAlaIleIleIleGlyPheAlaAlaLeu 213
              |||||||
Db   611 GACGCGGCCTGCGGGGTGGTGTTCCTGCTG 640
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RESULT 15
US-09-252-991A-9352/c
; Sequence 9352, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
;   SEQ ID NO 9352
;   LENGTH: 1650
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9352

Alignment Scores:
Pred. No.:   4.22e-16   Length: 1650
Score: 207.00   Matches: 58
Percent Similarity: 48.57%   Conservative: 44
Best Local Similarity: 27.62%   Mismatches: 92
Query Match: 18.24%   Indels: 16
DB: Gaps: 5

US-09-459-573-10 (1-223) x US-09-252-991A-9352 (1-1650)

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Db 1586 GTAGCCATGCAGGAATTGTCTGCTGCTGACCGTGGCGCGGTGTTCGCCATAGCCCTG 1527

Qy   32 PheAsnProGlyAlaAsnLeuPheValValGlnThrSerLeuAlaSerGlyLysArgArg 51
             :::||| ::: :::|||:::|||
Db 1526 GTCAGCCCGGTCCCGATGTCGCCCTGGTGGTGCACGGTCCCCTGCACCAGGGCGGCGGG 1467

Qy   52 AlaGlyValLeuThrGlyLeuGlyValAlaAlaLeuGlyValAspAlaPheTyrSerGlyLeuGly 71
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Db 1466 GCCGGCCTGGCCAGCGGCGTGGGGCTGGCCTGCGCGGGATTCTCTGCATACCACCCTGGTG 1407

Qy   72 LeuPheGlyLeuAlaThrLeuIleThrGlnCysGluGluIlePheSerLeuIleArgIle 91
           ||| :::|||
Db 1406 CTGACCGGCGGTGCTGCTGCGTGCTGCCAGCGTACGCCGTGTCAGCCTGGCTGGCTGG 1347

Qy   92 ValGlyGlyAlaTyrLeuLeuTrpPheAlaTrpCysSerMetArg---------ArgGln 108
           :::   :::|||
Db 1346 CTCGGCGGCCGCCTGTACCTGGCGCGCCTGGCTGGCTGGCCGGCGCCGGCGGGCGC 1287

Qy 109 SerThrProGlnMetSerThrLeuGln----------GlnProIleSerAlaPro 123
           :::||| :::
Db 1286 GGCGACGGCCAGCCGGCCGGCCACTGCCGGCGCCCCTG---GGGCCC 1230

Qy 124 TrpTyrValPhePheArgArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeu 143
           ||| :::|||:::
Db 1229 TGGCTG----------CGCGGAGTGGCGACCAATCTGTTCAATCCCAAGGCGCTGGTG 1182

Qy 144 PhePheSerIlePheSerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeu 163
             |||::: ||| :::|||
Db 1181 TTATTCATCGCCTTGCTCGGCAGCCTGATGTCGCTCGGCGGCCAAACTG 1122

Qy 164 MetAlaTrpAlaGlyIleIleValLeuAlaSerIleIleValPheGlyValPheGlnAla 183
             ||| :::|||
Db 1121 GCGGTGGCGGCGCTGCTGTTCGGCATGGGCGCCTGGTTCGGCCTGACC 1062
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us-09-459-573-10.rni

Wed Jan 26 08:14:34 2005

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Qy    184 PheSerLeuProAlaValArgArgAlaTyrGlyArgMetGlnArgValAlaSerArgVal 203
              :::   |||||||:::::::                      |||::: |||         :::
Db   1061 CTTACCCGCCCGGCCCTGCAG--------GCCCGCCTGTTGCGCGGTGCCCTGGCTG 1011

Qy    204 IleGlyAlaIleIleGlyValPheAlaLeu 213
              |||  |||||| |||
Db   1010 GACGCGGCCTGCGGGGTGGTGTTCCTGCTG 981
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Search completed: January 25, 2005, 13:41:53
Job time : 1364 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame plus p2n model

Run on: January 25, 2005, 12:28:08 ; Search time 378 Seconds
(without alignments)
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	225	19.8	1830121	14	US-10-329-960-1	Sequence 1, Appli
2	225	19.8	1830121	16	US-10-329-670-1	Sequence 1, Appli
3	225	19.1	1830121	18	US-10-158-865-1	Sequence 1, Appli
4	217	19.1	678	9	US-09-738-626-165	Sequence 165, App
5	217	19.1	3309400	9	US-09-738-626-1	Sequence 1, Appli
c 6	179	15.8	621		US-09-738-626-2918	Sequence 2918, Ap
c 7	179	15.6	3309400	9	US-09-738-626-1	Sequence 1, Appli
8	177.5	15.6	9025608	15	US-10-156-761-1	Sequence 1, Appli
9	175	15.4	651	15	US-10-156-761-3368	Sequence 3368, Ap
10	168	14.8	615	15	US-10-156-761-3747	Sequence 3747, Ap
11	168	14.8	32329	16	US-10-374-903A-1	Sequence 1, Appli
12	166	14.6	669	9	US-09-738-626-2570	Sequence 2570, Ap
13	166	14.6	792	10	US-09-746-660A-13	Sequence 13, Appl
14	166	14.4	799	18	US-10-494-672-295	Sequence 295, Appl
15	164	14.4	2731748	17	US-10-297-465A-1	Sequence 1, Appli
c 16	162	14.3	269223	16	US-10-672-787-41	Sequence 41, Appli
17	146.5	12.9	621	16	US-10-282-1222-41840	Sequence 41840, A
18	145	12.8	672	15	US-10-156-761-246	Sequence 246, App
19	143	12.6	630	16	US-10-282-122A-30630	Sequence 30630, A
20	141.5	12.5	621	16	US-10-282-122A-39598	Sequence 39598, A
21	138.5	12.2	618	16	US-10-282-122A-40780	Sequence 40780, A
22	135	11.9	633	16	US-10-282-122A-11642	Sequence 11642, A
23	134.5	11.9	623	16	US-10-282-122A-36679	Sequence 36679, A
c 24	134	11.7	86941	16	US-10-461-194-2	Sequence 2, Appli
25	133	11.7	618	16	US-10-282-122A-20027	Sequence 20027, A
c 26	133	11.4	85692	16	US-10-461-194-1	Sequence 1, Appli
c 27	129.5	11.4	820	13	US-10-194-163-142	Sequence 142, App
28	127.5	11.2	627	16	US-10-282-122A-14918	Sequence 14918, A
29	126.5	11.1	1200	9	US-09-927-395-1	Sequence 1, Appli
30	126.5	11.1	1200	9	US-09-847-392-1	Sequence 1, Appli
31	125	11.0	618	16	US-10-282-122A-23973	Sequence 23973, A
32	124.5	11.0	633	16	US-10-282-122A-31699	Sequence 31699, A
33	123.5	10.9	630	16	US-10-282-122A-33154	Sequence 33154, A
34	114	10.0	609	15	US-10-156-761-1109	Sequence 1109, App
35	109	9.6	623	9	US-09-974-300-366	Sequence 366, App
36	108.5	9.6	630	15	US-10-156-761-7444	Sequence 7444, Ap
c 37	104	9.2	9795	14	US-10-270-333-13	Sequence 13, Appl
38	101.5	8.9	750	16	US-10-520-487-1	Sequence 1, Appli
39	100.5	8.9	1893	16	US-10-282-122A-33782	Sequence 33782, A
40	100	8.8	543	16	US-10-282-122A-8689	Sequence 8689, Ap
41	96	8.5	633	16	US-10-282-122A-19891	Sequence 19891, A
42	95	8.4	636	16	US-10-282-122A-6905	Sequence 6905, Ap
43	93.5	8.2	1422	16	US-10-282-122A-25583	Sequence 25583, A
44	93	8.2	633	16	US-10-282-122A-23535	Sequence 23535, A
c 45	93	8.2	1234	16	US-10-425-114-20399	Sequence 20399, A

ALIGNMENTS

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; Sequence 1, Application US/10329960
; Publication No. US2003009277A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P1
; CURRENT APPLICATION NUMBER: US/10/329,960
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 1
; LENGTH: 1830121

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ORGANISM: Haemophilus influenzae
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Alignment Scores:
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Best Local Similarity: 26.09%
Query Match: 19.82%
DB: 14

Length: 1830121
Matches: 60
Conservative: 43
Mismatches: 87
Indels: 40
Gaps: 4

US-09-459-573-10 (1-223) x US-10-329-960-1 (1-1830121)

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Qy   133 IleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePheSerValThr 152
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Qy   173 SerIleIleTrpArgValPheLeuSerGlnAlaPheSerLeuProAlaValArgArgAla 192
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Qy   193 TyrGlyArgMetGlnArgValAlaSerArgValIleGlyAlaIleIleGlyValPheAla 212
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; Publication No. US20040018503A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fra
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P1
; CURRENT APPLICATION NUMBER: US/10/329,670
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
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Wed Jan 26 08:14:34 2005

us-09-459-573-10.rnpb

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Percent Similarity: 225.00          Matches:             60
Best Local Similarity: 44.78%       Conservative:        43
Query Match:        26.09%          Mismatches:          87
DB:                 19.82%          Indels:              40
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US-09-459-573-10 (1-223) x US-10-329-670-1 (1-1830121)

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Qy    24  ValGlyLeuPheValIleThrPheAsnLeuPheValValGln  43
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;  PRIOR APPLICATION NUMBER: US 09/557,884
;  PRIOR FILING DATE: 2000-04-25
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;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: US 08/426,787
;  PRIOR FILING DATE: 1995-04-21
;  NUMBER OF SEQ ID NOS: 1
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US-09-459-573-10 (1-223) x US-10-158-865-1 (1-1830121)

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Db 1385582  TACAGTCATACAGCCCGTTATATTGATAATATGCCAGGTATTGTATTTTTATTTTTGGT  1385641

Qy   213  LeuArgLeuIleTyrGluGlyValThrGln  222
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RESULT 4
US-09-738-626-165
; Sequence 165, Application US/09738626
; Publication No. US2002019760SA1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 165
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-165

Alignment Scores:
Pred. No.:   6.68e-17
Score: 217.00
Percent Similarity: 50.45%
Best Local Similarity: 28.64%
Query Match: 19.12%
DB:

Length: 678
Matches: 63
Conservative: 48
Mismatches: 81
Indels: 28
Gaps: 7

US-09-738-626-165 (1-678)

```
Qy    19  AlaValTyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeu  38
          ||:|:|||:||||                        :::::|||
Db    22  GGCCTTTTCTG------------GTGTGGATCGCAGCAATTGCATCCCCTGGGCCAGACCTT  72

Qy    39  PheValValGlnThrSerLeuAlaSerGlyValArgArgAlaGlyValLeuThrGlyLeu  58
          |||       ::::::|||    |||                         :::
Db    73  TTCCAGATCATCAGGCTAAGT--GCCAAAAACCGCCGTGATGGCTACTGACTGCCGTA  129

Qy    59  GlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeu  78
          |||    |||||            ::: ||| :::::
Db   130  GGCATCATGGTGGGAAACTCCATCTGATCATAGCCAGCCTCCTTGGGCTCTCGGCACTG  189

Qy    79  IleThrGlnCysGluGlyIleLeuPheSerLeuIleLeuValGlyGlyAlaTyrLeuLeu  98
          :|||:    |||:|||:||||                    ||||:|||
Db   190  ATCTCCACGTATCCAGCAATTTGAACCTGTTCAGCTCGTCGGTGGCGGTTATTGACC  249

Qy    99  TrpPheAlaTrpCysSerMetArg---------ArgGlnSerThrProGlnMetSer  114
          :::|||                           :::::|||||:
Db   250  TGGATGGGCATCGGCGGCGTGAGGTCATGGTGGACAAACGCTCCACACAGCAAGCTGCA  309

Qy   115  ThrLeuGlnGlnProIle-----------------------SerAlaProTrp  124
          ||||                                      |||
Db   310  GCGGATTCTCAAGCTGTAGAGAATACGTTGGTGACAGCCACGGCCACATCGTCGGAGTG  369

Qy   125  TyrValPhePheArgArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeuPhe  144
          |||||       |||:|:| :::|||    ||||:|:|||||
Db   370  TGGCCAGCTATTCGATCTGGCATTGCTACCAACTTGTCAACCCCAAAGCTGTGCTGTTT  429

Qy   145  PheIleSerIlePheSerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeuMet  164
          |||   |||     :::    :::     :::
Db   430  TTTGGTTCCGTTTTCGCCCAATTGTTAGACCTGACATGGAATCGGGTGGAGTATTTTC  489

Qy   165  AlaTrpAlaGlyIleValLeuAlaSerIleIleTrpArgValPheLeuSerGlnAlaPhe  184
          :::       |||          |||        |||
Db   490  ATTGGAGTCTTCCTCACCCTCACTGGCCTGCTGTCGGTTGTG----------GGGTTC  537

Qy   185  SerLeuProAlaValArgArgArgAlaTyrGlyArgMetGlnArgValAlaSerArgValIle  204
          :::                     :::    ||| :::              :|:||
Db   538  GCCGTCTTGGTCCGCAAACTAGCCGCTGGCCTCACCCGAAATGAGCC------ATCATC  591

Qy   205  GlyAlaIleIleGlyValPheAlaLeuArgLeu---------IleTyrGluGlyVal  220
          :::                    :|:          |||
Db   592  GACCTGCTAACGGGGGTGATTTCATCGGGCTGGGAAATGTTCATGATCTTCGAGGGGTT  651
```

RESULT 5
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US2002019760SA1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0

; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Alignment Scores:
Pred. No.:   3309400
Score: 1.5e-11
Percent Similarity: 50.45%
Best Local Similarity: 28.64%
Query Match: 19.12%
DB:

Score: 217.00
Matches: 63
Conservative: 48
Mismatches: 81
Indels: 28
Gaps: 9

US-09-459-573-10 (1-223) x US-09-738-626-1 (1-3309400)

```
Qy   19 AlaValTyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeu  38
         |||:||||||| |:|||:|:                       :::|||||:
Db 158175 GCGCTTTTTCTG---------GTGTGGATCGCAGCAATTGCATCCCTGGGCCAGACCTT 158225

Qy   39 PheValValGlnThrSerLeuAlaSerGlyArgArgAlaGlyValLeuThrGlyLeu  58
         ||||           :::|||:||:      ||||||||||||
Db 158226 TTCCAGATCATCAGGCTAAGT--GCCAAAAACCCGCGTGATGGGCTACTGACTGCCGTA 158282

Qy   59 GlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeu  78
         :::|||||||||:||:     :::       |||  |||||:|||:
Db 158283 GGCATCATCAGGTGGGAAACTCCATCTGGATCATAGACCAGCCTTCCTTGGGCTCCGCACTG 158342

Qy   79 IleThrGlnCysGluGluIlePheSerLeuIleArgIleValGlyLeuValGlyAlaTyrLeuLeu  98
         ||||:|||:|:::::|:||||:::::|||:||||:|||:|||||||    ||||||||||
Db 158343 ATCTCCACGATCCAGCAATTTGAACCTGTTGCAGCTCGTCGGTGGCGGTTATTTGACC 158402

Qy   99 TrpPheAlaTrpCysSerMetArg---------ArgGlnSerThrProGlnMetSer 114
         ||||         :::|||          :::|||||||||||    :::
Db 158403 TGGATGGGCATCGGGCGGTGAGGTCATGTGGACGAAACGCTCCACACAGCTGCA 158462

Qy  115 ThrLeuGlnGlnProIle----------SerAlaProTrp 124
         ||||  |||              |||
Db 158463 GCGGATTCTCAAGCTGTAGAGAATACGTTGGTGACAGCCACGGCTCATCGTCGGAGTG 158522

Qy  125 TyrValPheArgArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeuPhe 144
         ::|            |||||||||:||||||:|||:|||||||
Db 158523 TGGCCAGCTATTCGATCTGCATTGCTACCAACTGTCCAACCCCAAAGCTGTGCTGTTT 158582

Qy  145 PheIleSerIlePheSerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeuMet 164
         ||| |||:|||||||||:::            :::        :::
Db 158583 TTTGGTTCCGTTTCTTCGCCCCAATTTGTTAGACCTGACATGGGAATCGGGTGGAGTATTTTC 158642

Qy  165 AlaTrpAlaGlyIleValLeuAlaSerIleIleValAlaSerGlnAlaPhe 184
         :::|||     :::|||||||||||||||||||||    :::
Db 158643 ATTGGAGTCTTCCTCACCCTCACTCGGCTGTGTTGTG----------GGGTTC 158690

Qy  185 SerLeuProAlaValArgArgArgTyrGlyArgMetGlnArgValAlaSerArgValIle 204
         :::::::|||||         ||:||||||||||||||||    |||
Db 158691 GCCGTTCTTGGTCCGGCAAAGTAGCCCGCTGACCCTCACCCGAAATGAGCC------ATCATC 158744

Qy  205 GlyAlaIleIleGlyValPheAlaLeuArgLeu----------IleTyrGluGlyVal 220
         :::|||||||                |||:::||||||:
Db 158745 GACCTGCTAACGGGGGTGATTTTCATCGGGTGGGAATGTTCATGATCTTCGAGGGGGTT 158804
```

RESULT 6
US-09-738-626-2918

Alignment Scores:
Pred. No.:   621
Score: 3.05e-12
Percent Similarity: 179.00
Best Local Similarity: 47.09%
Query Match: 31.55%
DB: 15.77%

Length: 621
Matches: 65
Conservative: 32
Mismatches: 87
Indels: 22
Gaps: 9

US-09-459-573-10 (1-223) x US-09-738-626-2918 (1-621)

```
Qy   19 AlaValTyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeu  38
         |||:|||  |||           |||         |||
Db   28 GCACTCGCCATTATTGGTGGCATTAGCGGTG------------CCCGGACCTGACCTT  72

Qy   39 PheValValGlnThrSerLeuAlaSerGlyArgArgAlaGlyValLeuThrGlyLeu  58
         ||||   :::||||||||||||||||||||||||||||||||:::||||
Db   73 --GTTCTTGTTCTACATTCTGCAACCCGGGATCCGCACGGGGTCATGACTGCGGCA 129

Qy   59 GlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeu  78
         :::|||             :::|||:::       |||:|||:|||:
Db  130 GGAATCATGACGGACTGATGTTACATGCGAGCCGAGCAACTGCATTA 189

Qy   79 IleThrGlnCysGluGluIlePheSerLeuIleArgIleValGlyLeuValGlyAlaTyrLeuLeu  98
         ||||:::       :::|||:|||||:::||:|||||||:::
Db  190 TTGCTATCAGCTCCGGGAGTATTGAGCCTATTCAACTTCTTGGTGCGGAGTGCTTTTG 249

Qy   99 TrpPheAlaTrpCysSerMetArg---------ArgGlnSerThrProGlnMetGln 117
         :::                   :::::::||||||:::
Db  250 TGGATGGGCACGAACATGTTCGTGCTTCCCAAATACCGGGGAATCTGAAACTGCGCT 309

Qy  118 GlnProIleSerAlaProTrpTyrProValPhePheArgArgGlyLeuIleThrAspLeuSer 137
         :::         |||              |||:::
Db  310 AGTCAATGCAGTGCAGGTTATTTT------------CGAGGATTATCACCAATGCCACG 357

Qy  138 AsnProGlnThrValLeuPhePheIleSerIlePheSerValThrLeu---AsnAlaGlu 156
         :::||:||            :::|||:::::::||||||
Db  358 AACCCGAAAGCCGTCGGCTTGTTCTTTGCAGCGATTCTTCCTCAGTTCATTGGGAATGGGGAA 417

Qy  157 ThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIleValLeuAlaSerIleIleValAlaSerIleIleTrp 176
         :::|||                :::|||||||||||:::
Db  418 GATATGAAAAATGAGGACCCTTGGCATTGTGCCACCATCGTGCTTGGCTCAGGAGCGTGG 477

Qy  177 ArgValPheLeuSerGlnAlaPheSerLeuProAlaValArgArgArgTyrGlyArgMet 196
         :::                  ::
Db  478 TGGTTG------------------GGAACAATCGCATTGGTCAGGGGTATTGGT---CTG 516

Qy  197 GlnArgVal------AlaSerArgValIleGlyValPheAlaLeuArg 214
         :::|||        |||::|||||||||||||
Db  517 CAAAAGTTACCGTCTGCGGGATCGCATTATC---ACCCTGGTTGGTGGTGCATCGCCACTGTTT 573

Qy  215 LeuIleTyrGluGlyVal 220
         |||:::||:||||||||||
Db  574 CTCATTGGTGCCGGATTA 591
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RESULT 7
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Alignment Scores:
Pred. No.:   3309400
Score: 7.81e-07   Matches: 65
Percent Similarity: 179.00   Conservative: 32
Best Local Similarity: 47.09%   Mismatches: 87
Query Match: 31.55%   Indels: 22
DB: 15.77%   Gaps: 9

US-09-459-573-10 (1-223) x US-09-738-626-1 (1-3309400)

Qy   19 AlaValTyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeu 38
         ||:| :: |||
Db 2826808 GCACTCGCATTATTGGTGGCATTAGCGGTG----------CCCGGACCTGACCTT 2826764

Qy   39 PheValValGlnThrSerLeuAlaSerGlyArgArgAlaGlyValLeuThrGlyLeu 58
         ||:|:||| ||| :|||||
Db 2826763 --GTTCTTGTTCTACATTCTGCAACCCGCGGATCCCACCGGGGTCATGACTGCCGCA 2826707

Qy   59 GlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeu 78
         |||:|| :|:::|| ||| |||
Db 2826706 GGAATCATGACGGACTGATGTTACATGCGAGTCTTGCGATAGCCGGAGCAACTGCATTA 2826647

Qy   79 IleThrGlnCysGlyLeuIlePheSerLeuIleArgIleValGlyValAlaTyrLeuLeu 98
         ||| ||||:|||| |||:||
Db 2826646 TTGCTATCAGCTCCGGAGTATTGAGCGCTATTCAACTTCTTGGTGCGGAGTGCTTTTG 2826587

Qy   99 TrpPheAlaTrpCysSerMetArg--ArgGlnSerThrProGlnMetSerThrLeuGln 117
         ::||| ||| :|:
Db 2826586 TGGATGGGCACGAACATGTTTCGTGCTTCCCAAAATACCGGGAATCTGAAACTGCTGCT 2826527

Qy   118 GlnProIleSerAlaProTrpTyrValPhePheArgArgArgLeuIleThrAspLeuSer 137
         |||||| :|| |||:|: :::
Db 2826526 AGTCAATCGAGTGCAGGTTATTT-----------CGAGGATTTATCACCAAATGCCACG 2826479

Qy   138 AsnProGlnThrLeuPhePheIleSerIlePheSerValThrLeu---AsnAlaGlu 156
         ||| |||:||||| :::|||
Db 2826478 AACCCGAAAGCCGCTGTTGTTCTTTGCAGCGATTCTTCCTCAGTTCATTGGAATGGGAA 2826419

Qy   157 ThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyAlaGlyIleValIleAlaSerIleIleTrp 176

Db 2826418 GATATGAAAATGAGGAACCTTGGCATTGTGTGCCACCATCGTCGTTGGCTCAGGAGCGTCG 2826359
          ||| ||| |||

Qy   177 ArgValPheLeuSerGlnAlaPheSerLeuProAlaValArgAlaTyrGlyArgMet 196
         :::
Db 2826358 TGGTTG--------------------------GGAACAATCGCATTGGTCAGGGTATTGGT---CTG 2826320

Qy   197 GlnArgVal-----AlaSerArgValIleGlyValAlaIleIleGlyValPheAlaLeuArg 214
         |||:|::| ::|||:|||
Db 2826319 CAAAAGTTACCGTCTGCCGATCCCATTATC--ACCCTGGTTGGTGGCATCGCACTGTTT 2826263

Qy   215 LeuIleTyrGluGlyVal 220
         ||||| |:::
Db 2826262 CTCATTGGTGCCGGATTA 2826245

RESULT 8
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US2003011901841
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Alignment Scores:
Pred. No.:   9025608
Score: 5.14e-06   Matches: 64
Percent Similarity: 177.50   Conservative: 35
Best Local Similarity: 43.42%   Mismatches: 102
Query Match: 28.07%   Indels: 27
DB: 15.64%   Gaps: 9

US-09-459-573-10 (1-223) x US-10-156-761-1 (1-9025608)

Qy   8 PheMetAspGluIleThrMetAspProLeuHisAlaValTyrLeuThrValGlyLeuPhe 27
         ||:||| ::||| |||
Db 4202015 TTCATGTTTGGTGTCACCGATCTCCCC-------ACCTACCTC---GCAGGCCTTGTC 4201968

Qy   28 ValIleThrPhePheAsnProGlyAlaAsnLeuPheValValGlnThrSerLeuAla 47
         :::|| :::
Db 4201967 CTGATCGTCCTGCTC---CCCGGTCCGACTCCGCTGTACGTGTTGTCCGCGCCCGGC 4201911

Qy   48 SerGlyArgArgAlaGlyValLeuThrGlyLeuGlyLeuPheGlyLeuAlaLeuGlyAspAlaPheTyr 67
         ||||| ||||| ||:||
Db 4201910 AAGGGGCTACGCGCGGATACACGGCAGCCGCCGCGTCGGTGCGGTGACACCGTGCTG 4201851

Qy   68 SerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGluGluPheSer 87
         ||| |||:||:||| ::|||
Db 4201850 ATGACGGTCTCCGGCCGGGAGTGCCGTGCGCTGCCTGCTGCTCCAGGCGAACGACCCTGCTGTTCGGG 4201791

Qy   88 LeuIleArgIleValGlyValAlaTyrLeuLeuTrpPheAlaTrpCysSerMetArg--- 106

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Db      28  TACCTC---GCAAGGCCTTGTCCTGATCGTCCTCGCTC---CCCGGTCCGGAACTCGCTGTAC  81
                :::    ||||||    |||             |||              :::||||
Qy      41  ValValGlnThrSerLeuAlaSerGlyArgArgAlaGlyValLeuThrGlyLeuGlyVal      60

Db      82  GTGTTGTCCGTCGCGCCCCGCCAAGGGCGTACGCGCCGGATACACCGGCAGCGGCGGCGTC    141
                |||    :::               |||::::::||||
Qy      61  AlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIleThr      80

Db     142  TGGTGCGGTGACACCGTGTATGACGCTGTCCGCGGCGAGTCGCCTCGCTGCTCCAG         201
                |||    :::                 |||:::||||
Qy      81  GlnCysGluGluIlePheSerLeuIleArgIleValGlyAlaTyrLeuLeuTrpPhe       100

Db     202  GCGAACGCCCTGCTGTTCGGGATCGTGAAGTCGAAGTACGCCGGGGGGTATCGTCGACTTGGCTC  261
                :::||||               :::::::
Qy     101  AlaTrpCysSerMetArg----------ArgGlnSerThrProGlnMetSer            114

Db     262  GCGGTTCGGCATGCTGCGGGCCGGGTGGCGGACCCGCCGGGAGATGTGGCGGACGGCGGAC    321
                ||||
Qy     115  ThrLeuGlnGlnProIleSer-----------AlaProTrpTyrValPhePheArg        129

Db     322  GCGGCCCGGGCACCCGTCGCCGGAGAGCGGCC------------TTCCGG               369
                :::||||:::
Qy     130  ArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeuPhePheSerIlePhe       149

Db     370  CGGGGCGTTCGTCGTCAGCCTCTTCAACCCGAAGGCGATCCTGTTCGTCCGCCTTCTTC     429
                |||||||||              :::||||
Qy     150  ------SerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpAla    167

Db     430  GTTCAGTTCGTCGACCCGGGGTACGCCTACCCGGTCCTGTTCCTGTACCGCGCTG-----ATCTTCAGCGGCCACG  489
                ||||||||              :::::::
Qy     168  GlyIleValLeuAlaSerIleIleTrpTyrArgValPheLeuSerGlnAlaPheSerLeuPro 187

Db     490  TTCGCCCAGCTGGCGAGCTTCCTGTACCTCACCGCCCGCTG-----ATCTTCAGCGACGGCCACG 543
                :::::::
Qy     188  AlaValArgArgAlaTyrGlyArgMetGlnArgVal--------AlaSerArgValIle      204

Db     544  AAGCTGGCGGCGCCGCTCCGCGACGCAGCGGGTCTTCCGCGGGGCCACGACCGCCGCCG     603
                |||:::
Qy     205  GlyAlaIleIleGlyValPheAlaLeuArgLeuIleTyrGluGly                   219

Db     604  GGGGCCCTCTTCCTGGGGCTTCGCCGTGAAGCTGACACTGGCCGGC                  648
```

Alignment Scores:

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Db  4201790  ATCGTGAAGTACGCCGGGGCCGGGTATCTGACCTCGCCTTCGGCATGCTGCGGGCC  4201731
                 :::::::::::              |||:::          |||
Qy      107  ------------ArgGlnSerThrProGlnMetSerThrLeuGlnGlnProIleSer      121

Db  4201730  GGCGTGGGAGATGTGGCGGACCCGCCGGAGACGGCGCCCGTCGCG             4201671
                 |||||||                  :::                 |||:::::::|||
Qy      122  ------------AlaProTrpTyrValPhePheArgArgGlyLeuIleThrAspLeu      136

Db  4201670  CCGGTCGCCGGAGAGCGGGCCC-----------TTCCGGCGGGGTTCGTCGTCAGCCTC  4201623
                                   :::
Qy      137  SerAsnProGlnThrValLeuPhePheSerIlePhe------SerValThrLeuAsn     154

Db  4201622  TTCAACCCGAAGGCGATCCTGTTCGTCCGCCTTCTTCGTTCAGTTCGTCGACCCGGGG  4201563
                 ||||||||:::::::||
Qy      155  AlaGluThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIleValLeuAlaSerIle  174

Db  4201562  TACGCCTACCCGCCCTTCGTTCCTCCGGCCTTCGCCCAGCTGGCGAGCTTC         4201503
                 ||||||    :::::::
Qy      175  IleTrpTyrArgValPheLeuSerGlnAlaPheSerLeuProAlaValArgArgAlaTyrGly  194

Db  4201502  CTGTACCTCACCGCCGCTG-----ATCTTCAGCGACGAAGCTGGCGGCGCCCTTCCGC  4201449
                 |||:::||||:::                 :::  |||
Qy      195  ArgMetGlnArgVal-------AlaSerArgValIleGlyAlaIleIleGlyValPhe     211

Db  4201448  CGACGCAAGCGGCCTCCGCGGGAGCCCACGACCGCGCCGCCCTCTTCCTGGGCTTC     4201389
                 |||:::||||:::
Qy      212  AlaLeuArgLeuIleTyrGluGly                                        219

Db  4201388  GCCGTGAAGCTGACACTGGCCGGC                                    4201365
                 |||
```

Alignment Scores:

Pred. No.:		
Score:	1.03e-11	175.00
Percent Similarity:	43.72%	
Best Local Similarity:	27.91%	
Query Match:	15.42%	
DB:		

Length:	651	
Matches:	60	
Conservative:	34	
Mismatches:	97	
Indels:	24	
Gaps:	8	

US-09-459-573-10 (1-223) x US-10-156-761-3368 (1-651)

```
Qy      21  TyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheVal   40
                 ||||||              :::|||                         |||
```

Wed Jan 26 08:14:34 2005

us-09-459-573-10.rnpb

US-10-374-903A-1

```
Alignment Scores:
Pred. No.:
Score:                 2.19e-08        Length:              32329
                       168.00          Matches:             60
Percent Similarity:    40.93%          Conservative:        37
Best Local Similarity: 25.32%          Mismatches:          98
Query Match:           14.80%          Indels:              42
DB:                    16              Gaps:                8
```

US-09-459-573-10 (1-223) x US-10-374-903A-1 (1-32329)

```
Qy     6 HisLeuPheMetAspGluIleThrMetAspProLeuHisAlaValTyrLeuThr---Val  24
           |||       ::|    |||||||:|:|||||   :|:
Db  4093 CACCGTGCGTTCGCGCGCCCACGATGGAGCCCATGTCCACCACCGCACTCGGCGTTCCTC 4152

Qy    25 GlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValValGlnThr  44
           |||||            ||:           :::::::::::
Db  4153 GGGCGGCTCGCGTGCTGATCGCCGCGCCCGGTCCCAGCACGATGTCATCATCCGGCCAG 4212

Qy    45 SerLeuAlaSerGlyArgArgAlaGlyValLeuThrGlyLeuGlyValAlaLeuGlyAsp  64
           |:|||||      |||||  :||| :||||||||
Db  4213 TCGCTGCACAGC---AGACGGGCCGGTTCCTGACCGTTCTGGGCAACGAGACCGGGGTG 4269

Qy    65 AlaPheTyrSerGlyLeuGlyLeuPheGlyLeuLeuAlaThrLeuIleThrGlnCysGluGlu  84
             :::       |||||||||||||   |||:||
Db  4270 CTCACCTGGCGGTGGTGGCGGGCCGGTGGCGCTGACCGGCGTGCTGGCCGCCTCCCGCACG 4329

Qy    85 IlePheSerLeuIleArgIleValGlyIleValGlyGlyGlyGlyIleAlaTyrLeuLeuTrpPheAlaTrpCysSer 104
           :::        |||||||||            :::
Db  4330 GCCTACGACACGTGATGCGGATCGGCGGGGCGCGGGGGGGCGGTGGTGGTACGGCGTGCAGACG 4389

Qy   105 MetArg------------------ArgGlnSerThrProGlnMetSerThrLeuGln 117
           :::||
Db  4390 CTGCGGGCCCGCGCCCGGCGGAGGCAGCACGGGCCCTCCGCGCCGACGAGGGCGGCGGTG 4449

Qy   118 GlnProIleSerAlaProTrpProTyrValPhePheValPheAlaArgGlyLeuIleThrAspLeuSer 137
           |||||      :::        :|||||:|::
Db  4450 GTGCCCCGTTCCGGC---TGGAAGATC---TACCGGTCCGGCGTCGCTGCTCAACCTCGCC 4503

Qy   138 AsnProGlnThrValLeuPhePheIleSerIlePheSerValThrLeuAsnAlaGluThr 157
           |||          ||::|:        :::|
Db  4504 AACCCCAAGGCGCCGTCTTCGCCATGTCCTTCCGTCCGCCAGTTCGTCCCGGCCGGTCCG 4563

Qy   158 ProThrTrpAlaArgLeuMetAlaTrpAlaGlyIle------------Val 170
           :::                      :::
Db  4564 CCCAAGCTGCCGGTGATCACCGGCGCTCGCCGCGTTCCAGGCGCTCTTCGAGGTCGGGTAC 4623

Qy   171 LeuAlaSerIleIleTrpArgValPheArgValPheLeuSerGlnAlaPheSerLeuProAlaValArg 190
           ::|||                  |||
Db  4624 TACGGGATGTACGTGTGGTTCGTC-------------------------------------- 4647

Qy   191 ArgAlaTyrGlyArgMetGlnArgValAlaSerArg--------------------- 202
           |||||                :::::|||||
Db  4648 -------GGCCGGATGAAGAGGGTGATCTCCGGGGGCGCGGCGGCCGCCGGCGGCTGAG 4698

Qy   203 ---ValIleGlyAlaIleIleGlyValPheAlaLeuArgLeuIleTyrGlu 218
              ::|        |||:  :::        :::|
Db  4699 CAGGTGTCGGGGGCGTGCTCGTGCTCGGCGATCCGGATCGGGCATCCGGATGGCGGTCGAG 4749
```

RESULT 12
US-09-738-626-2570

```
Pred. No.:
Score:                 6.98e-11        Length:              615
                       168.00          Matches:             52
Percent Similarity:    45.27%          Conservative:        39
Best Local Similarity: 25.87%          Mismatches:          90
Query Match:           14.80%          Indels:              20
DB:                    15              Gaps:                8
```

US-09-459-573-10 (1-223) x US-10-156-761-3747 (1-615)

```
Qy    19 AlaValTyrLeuThrValGlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeu  38
           |||       ::|||| |||    :::::   |||      ||||||||
Db    19 GCGGCCTTCCTGGCGATTGATCTTCTGCTGGTG------TTCACGCCCGGGGCCGGACTGG  72

Qy    39 PheValValGlnThrSerLeuAlaSerGlyArgArgAlaGlyAlaGlyLeuThrGlyLeuLeu  58
           |||                                  ::|
Db    73 GCCTACGCGATCGGCGGCGGGGACTCGCGGGAC-------CGTTCGGTCGTCCCGGCGGTGGCC 126

Qy    59 GlyValAlaLeuGlyAspAlaPheTyrSerGlyLeuGlyLeuPheGlyLeuLeuAlaThrLeu  78
           |||:::       |||            |||:::        ||||||     :::|
Db   127 GGGCTGGTGGGCGGGGATCACGCCCGGGTACACCCCTGCTCCGCCGGCCGGCTGGTGGTGATC 186

Qy    79 IleThrGlnCysGluGluIlePheSerLeuIleLeuPheSerLeuLeuIleArgIleValGlyIleValGlyAlaTyrLeuLeu  98
           ::| ||          :::|||::|                       ||||||||:::
Db   187 GTCGCCGGCTCCCGCGAGCCTGCTACCGCCTGACCGTCCTGGGGGGCCGCCTACCTGATA 246

Qy    99 TrpPheAlaTrpCysSerMetArgGlnSerThrProGlnMetSerThrLeuGlnGln 118
           |||                  ::|||||||||| |||
Db   247 TGGCTCGGCTGGAGCGTTCTGGCCGGCGGGGACTCCCCAGGCCGCCACTCCCGCG---GAGGCC 303

Qy   119 ProIleSerAlaProTrpProTyrValPhePheValPheArgGlyLeuIleThrAspLeuSerAsn 138
           |||           ::: |||       :::|||:::
Db   304 GTGGCCGGCTTCCAGGTGGCGGATCGTGCTGAGGGGCCGGGGGGATCAGCCGGTCTG---AAC 360

Qy   139 ProGlnThrValLeuPhePheIleSerIlePheSerValThrLeuAsn------------- 154
           |||||          |||||::|
Db   361 CCCAAGGCCGTGCTGCTGTACTTCTCTGTTCCCGCAGTTCATCCACCCCGGTGAGGGG 420

Qy   155 --------------AlaGluThrProThrTrpAlaArgLeu---MetAlaTrpAlaGlyIle 169
                         ::: |||       :::
Db   421 TGGCCCGTAGCGGCTCAGACACCGGTCGTTCGGCACGCTCACCATGGCCAGCTGCGCCGTC 480

Qy   170 Val------LeuAlaSerIleIleTrpArgValPheArgValPheLeuSerGlnAlaPheSerLeuPro 187
           |||                  ::: |||
Db   481 GTCTACCTGGCCCGTGGCGTTTGGCCCGCACCGTACTGAAG-------GCCCGGCCG 531

Qy   188 AlaValArgArgAlaTyrGlyArgMetGlnArgValAlaSerArgValIleGlyAlaIle 207
           |||||              |||
Db   532 ACGGCGGCGCTCGCCGCCCGTGGCCCGGAGTCAGCGGAACCATGATGATCGTCATCGGCGGGTTC 591

Qy   208 Ile 208
           |||
Db   592 CTC 594
```

```
; Sequence 2570, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWA, SATOSHI
;   APPLICANT: MIZOGUCHI, HIROSHI
;   APPLICANT: ANDO, SEIKO
;   APPLICANT: HAYASHI, MIKIRO
;   APPLICANT: OCHIAI, KEIKO
;   APPLICANT: YOKOI, HARUHIKO
;   APPLICANT: TATEISHI, NAOKO
;   APPLICANT: SENOH, AKIHIRO
;   APPLICANT: IKEDA, MASATO
;   APPLICANT: OZAKI, AKIO
;   TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;   FILE REFERENCE: 249-125
;   CURRENT APPLICATION NUMBER: US/09/738,626
;   CURRENT FILING DATE: 2000-12-18
;   PRIOR APPLICATION NUMBER: JP 99/377484
;   PRIOR FILING DATE: 1999-12-16
;   PRIOR APPLICATION NUMBER: JP 00/159162
;   PRIOR FILING DATE: 2000-04-07
;   PRIOR APPLICATION NUMBER: JP 00/280988
;   PRIOR FILING DATE: 2000-08-03
;   NUMBER OF SEQ ID NOS: 7059
;   SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2570
;   LENGTH: 669
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-2570

Alignment Scores:
Pred. No.:                1.4e-10      Length:           669
Score:                    166.00       Matches:          57
Percent Similarity:       49.31%       Conservative:     50
Best Local Similarity:    26.27%       Mismatches:       80
Query Match:              14.63%       Indels:           30
DB:                                    Gaps:             8

US-09-459-573-10 (1-223) x US-09-738-626-2570 (1-669)

Qy      26 LeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValValGlnThrSer 45
              |||  :: ::||||| |::  :::  ||  ::  :::::::
Db      34 CTCAATTTGGTGGGCAGTTTATCCCCGGGGCCTGATACCTTTTTCCTCCTCCGC------ 87

Qy      46 LeuAlaSerGlyArgArgAlaGlyValLeuThrGlyLeu---GlyValAlaLeuGlyAsp 64
              ||||||           |::  :  |||  |::::
Db      88 TTAGCCACCCGCTCCAGAGCGCACCGGATCGCTGGCGTGCCGCATCGTCACCGGACTC 147

Qy      65 AlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrGlnCysGluGlu 84
              ||:   : :  || ||:  ||::|:|||
Db     148 ACGGTGTGGGTGACGCTGACGGTCGTGGGAGCAGCGGCGGCTGCTCACCACTTATCCGTCG 207

Qy      85 IlePheSerLeuIleArgIleValGlyIleValAlaTyrLeuLeuTrpPheAlaTrpCysSer 104
              |||  :::::||::::::||||||||        :: ::
Db     208 ATTCTCGGAATCATCCAGCTCGTCGGCGCGCACGTACCTAAGCTTCATTGGGTACAAGTTG 267

Qy     105 MetArgArgGlnSerThrProGlnMetSerThrLeuGln-------------------- 117
              |||  :: :||:
Db     268 CTGCGCCTCCGGCGTCGAGAGACTTATCGACGCCCCAGTTCGTTTCAACGCCGATGCC 327

Qy     118 GlnProIleSerAlaProTrpTyrVal------------------------PhePheArg 129
              ::||||||                                          :: |||
Db     328 CGACCTATC------CCGGATGCGGTAGAAGCACTGGGAACCCGCACTCAGTATATCGA 381

Qy     130 ArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePhe 149
              :::|||||:  || |||||:::::::||  ::::|||::   ::||
Db     382 CAAGGTTTGGCCACCAACCTGTCAAACCCTAAAGTTGTCATGTACTTCGCGGCAATTCTG 441

Qy     150 SerValThrLeuAsnAlaAlaGluThrProThrAlaArgLeuMetAlaTrpAlaGlyIle 169
              :::  :|||||                  :: :::::
Db     442 GCTCCGGTGCTGTGGGGTTCTCT------TCACCGGGTGCTGGCGTCTT 486
```

```
Qy     170 ValLeuAlaSerIleIleTrpArgValPheLeuSerGlnAla-----------Phe 184
              :::::  :|| |||  :::|| :::::: |||:::  ||:::
Db     487 ATCATCGTGGCGCCGGATTTTAGTGCAGACCTTTGTTACCTTCTGTGCTGCCTCATTGTC 546

Qy     185 SerLeuProAlaValArgArgAlaTyrArgAlaArgMetGlnArgValAlaSerArgValIle 204
              |||      |||::  :::||||  :::::||||| :::
Db     547 TCTACGGAGCGTGCGCAAAGCAATGCTGCGTGAGAGGTCCTGGTTGACCTGCTTGCT 606

Qy     205 GlyAlaIleIleGlyValPheAlaLeuArgLeuIleTyrGluGlyValGlyValThr 221
              |||   ::: ::  |||     ::  :|:
Db     607 GGCGTTGCTTGCTTCCTCCGTGTGGGTGTGACTCTGCTCGTATGAAGGCCTGACC 657
```

```
RESULT 13
US-09-746-660A-13
; Sequence 13, Application US/09746660A
; Publication No. US20030049804A1
; GENERAL INFORMATION:
;   APPLICANT: Pompejus, Markus
;   APPLICANT: Kroger, Burkhard
;   APPLICANT: Schroder, Hartwig
;   APPLICANT: Zelder, Oskar
;   APPLICANT: Haberhauer, Gregor
;   APPLICANT: Kim, Jun-Won
;   APPLICANT: Lee, Heung-Schick
;   APPLICANT: Hwang, Byung-Joon
;   TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
;   TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
;   FILE REFERENCE: BGI-121CP2
;   CURRENT APPLICATION NUMBER: US/09/746,660A
;   CURRENT FILING DATE: 2000-12-22
;   PRIOR APPLICATION NUMBER: 09/606740
;   PRIOR FILING DATE: 2000-06-23
;   PRIOR APPLICATION NUMBER: 09/603124
;   PRIOR FILING DATE: 2000-06-23
;   PRIOR APPLICATION NUMBER: 60/141031
;   PRIOR FILING DATE: 1999-06-25
;   PRIOR APPLICATION NUMBER: 60/142101
;   PRIOR FILING DATE: 1999-07-02
;   PRIOR APPLICATION NUMBER: 60/148613
;   PRIOR FILING DATE: 1999-08-12
;   PRIOR APPLICATION NUMBER: 60/187970
;   PRIOR FILING DATE: 2000-03-09
;   PRIOR APPLICATION NUMBER: DE 19931420.9
;   PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 125
;   SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 13
;   LENGTH: 792
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(769)
;   OTHER INFORMATION: RXC02390
US-09-746-660A-13

Alignment Scores:
Pred. No.:                1.78e-10     Length:           792
Score:                    166.00       Matches:          57
Percent Similarity:       49.31%       Conservative:     50
Best Local Similarity:    26.27%       Mismatches:       80
Query Match:              14.63%       Indels:           30
DB:                                    Gaps:             8

US-09-459-573-10 (1-223) x US-09-746-660A-13 (1-792)

Qy      26 LeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValValGlnThrSer 45
              |||  :: ::|||||  ::  :::  ||  ::
Db     134 CTCAATTTGGTGGGCAGTTTATCCCCGGGGCCTGATACCTTTTTCCTCCTCCGC------ 187

Qy      46 LeuAlaSerGlyArgArgAlaGlyValLeuThrGlyLeu---GlyValAlaLeuGlyAsp 64
              ||||||           |::  :  |||
Db     188 TTAGCCACCCGCTCCAGAGCGCACCGGATCGCTGGCGTGCCGCATCGTCACCGGACTC 247
```

DB:

US-09-459-573-10 (1-223) x US-10-494-672-295 (1-799)

Score: 18   Gaps: 8

```
Qy   26  LeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValValGlnThrSer  45
             ::::::|||       :::|||||   ::  :||||   :::::::
Db  134  CTCAATTGGTGGGCAGTTATCCCCGGGGCCTGATACCTTTTTCCTCCTCCGC------  187

Qy   46  LeuAlaSerGlyArgArgAlaGlyAlaGlyValLeuThrGlyLeu--GlyValAlaLeuGlyAsp  64
             |||||||   ::    :::::|||:::   |||:::   |||
Db  188  TTAGCCACCCGCTCCAGAGCGCACGCGATCCTGGCGTCGCCCGGCATCGTCACCGGACTC  247

Qy   65  AlaPheTyrSerGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGluGlu  84
             ::|||    |||   |||   |||   |||:::|||
Db  248  ACGGTGTGGGTGACGCTGACGGTCGTGGGAGCAGCGGCCGCCTGCTCACCACTTATCCGTCG  307

Qy   85  IlePheSerLeuIleArgIleValGlyValGlyValAlaTyrLeuLeuTrpPheAlaTrpCysSer  104
             :::::|||||     :::|||||:::   :::   :::
Db  308  ATTCTCGGAATCATCCAGCTCGTCGGGGGCACGTACCTTAAGCTTCATTGGGTACAAGTTG  367

Qy  105  MetArgArgGlnSerThrProGlnMetSerThrLeuGln  117
             :::|||||   :::
Db  368  CTGCGCTCGGCGTCGGAGAGACTTATCGACGCCCCAGTTCCGTTCAACCGCCGATGCC  427

Qy  118  GlnProIleSerAlaProTrpTyrVal----------------PhePheArg  129
             :::|||||       :::|||
Db  428  CGACCTATC------CCGGATGCGGTAGAAGCACTGGGAACCCGCACTCAGGTATATCGA  481

Qy  130  ArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePhe  149
             ::|||||||     :::   ::
Db  482  CAAGGTTTGGCCACCAACCTGTCAAACCCTAAAGTTGTCATGTACTTCGCGGCAATTCTG  541

Qy  150  SerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIle  169
             :::   :::::::|||:::
Db  542  GCTCCGGTTGATGCCAGCGCACCCA--------TCACCGGTGCTGGCGTTCTCT------  586

Qy  170  ValLeuAlaSerIleIleTrpArgValPheLeuSerGlnAla-------------Phe  184
             :::|||::  ::  :::
Db  587  ATCATCGTGGCGATTTTAGTGCAGACCTTTGTTACCTTCTCTGCTGTGCCTCATTGTC  646

Qy  185  SerLeuProAlaValArgArgAlaTyrGlyArgMetGlnArgValAlaSerArgValIle  204
             |||                        :::|||
Db  647  TCTACGGAGCGTGTGCGCAAAGCAATGCTGCGTGCAGGTCCCTGGTTTGACCTGCTTGCT  706

Qy  205  GlyAlaIleIleGlyValPheAlaLeuArgLeuIleTyrGluGlyValThr  221
             :::|||        :::   |||||||||:::|||
Db  707  GGCGTTGTCTTCCTCGGTTGTGGGTGACTCTGCTGTATGAAGGCCTGACC  757
```

RESULT 15
US-10-297-465A-1

; Sequence 1, Application US/10297465A
; Publication No. US20040142413A1
; GENERAL INFORMATION:
; APPLICANT: Simpson, Andrew
; APPLICANT: Reinach, Fernando
; APPLICANT: Setubal, Joao
; APPLICANT: Medianis, Joao
; APPLICANT: Arruda, Paulo
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: Isolated Genome of Xylella Fastidiosa and Uses Thereof
; FILE REFERENCE: FAPESP 202 US (10213376)
; CURRENT APPLICATION NUMBER: US/10/297,465A
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: PCT/IB01/01618
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,906
; PRIOR FILING DATE: 2001-06-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2731748
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-297-465A-1

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us-09-459-573-10.rnpb

```
Qy   65  AlaPheTyrSerGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGluGlu  84
             :::|||       ::    |||   :::|||
Db  248  ACGGTGTGGGTGACGCTGACGGTCGTGGGAGCAGCGGCCGCCTGCTCACCACTTATCCGTCG  307

Qy   85  IlePheSerLeuIleArgIleValGlyValGlyValAlaTyrLeuLeuTrpPheAlaTrpCysSer  104
             :::::|||||     :::|||:::   :::
Db  308  ATTCTCGGAATCATCCAGCTCGTCGGGGGCACGTACCTTAAGCTTCATTGGGTACAAGTTG  367

Qy  105  MetArgArgGlnSerThrProGlnMetSerThrLeuGln  117
             :::|||||   :::
Db  368  CTGCGCTCGGCGTCGGAGAGACTTATCGACGCCCCAGTTCCGTTCAACCGCCGATGCC  427

Qy  118  GlnProIleSerAlaProTrpTyrVal----------------PhePheArg  129
             :::|||||       :::|||
Db  428  CGACCTATC------CCGGATGCGGTAGAAGCACTGGGAACCCGCACTCAGGTATATCGA  481

Qy  130  ArgGlyLeuIleThrAspLeuSerAsnProGlnThrValLeuPhePheIleSerIlePhe  149
             ::|||||||     :::   ::
Db  482  CAAGGTTTGGCCACCAACCTGTCAAACCCTAAAGTTGTCATGTACTTCGCGGCAATTCTG  541

Qy  150  SerValThrLeuAsnAlaGluThrProThrTrpAlaArgLeuMetAlaTrpAlaGlyIle  169
             :::   :::::::|||:::
Db  542  GCTCCGGTTGATGCCAGCGCACCCA--------TCACCGGTGCTGGCGTTCTCT------  586

Qy  170  ValLeuAlaSerIleIleTrpArgValPheLeuSerGlnAla-------------Phe  184
             :::|||::  ::  :::
Db  587  ATCATCGTGGCGATTTTAGTGCAGACCTTTGTTACCTTCTCTGCTGTGCCTCATTGTC  646

Qy  185  SerLeuProAlaValArgArgAlaTyrGlyArgMetGlnArgValAlaSerArgValIle  204
             |||                        :::|||
Db  647  TCTACGGAGCGTGTGCGCAAAGCAATGCTGCGTGCAGGTCCCTGGTTTGACCTGCTTGCT  706

Qy  205  GlyAlaIleIleGlyValPheAlaLeuArgLeuIleTyrGluGlyValThr  221
             :::|||        :::   |||||||||:::|||
Db  707  GGCGTTGTCTTCCTCGGTTGTGGGTGACTCTGCTGTATGAAGGCCTGACC  757
```

RESULT 14
US-10-494-672-295

; Sequence 295, Application US/10494672
; Publication No. US20050003494A1
; GENERAL INFORMATION:
; APPLICANT: Zelder, Oskar
; APPLICANT: Pompejus, Markus
; APPLICANT: Schroder, Hartwig
; APPLICANT: Kroger, Burkhard
; APPLICANT: Klopprogge, Corinna
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: Genes coding for novel proteins
; FILE REFERENCE: BGI 16PUS
; CURRENT APPLICATION NUMBER: US/10/494,672
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: PCT/EP02/12134
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: DE 10154177
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 434
; SEQ ID NO 295
; LENGTH: 799
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(769)
; OTHER INFORMATION: RXA02390
US-10-494-672-295

Alignment Scores:
Pred. No.:   1.81e-10
Score: 166.00
Percent Similarity: 49.31%
Best Local Similarity: 26.27%
Query Match: 14.63%

Length: 799
Matches: 57
Conservative: 50
Mismatches: 80
Indels: 30

```
Alignment Scores:
Pred. No.:              4.3e-05         Length:          2731748
Score:                  164.00          Matches:         45
Percent Similarity:     52.70%          Conservative:    33
Best Local Similarity:  30.41%          Mismatches:      56
Query Match:            14.45%          Indels:          14
DB:                     17              Gaps:            4

US-09-459-573-10 (1-223) x US-10-297-465A-1 (1-2731748)

Qy         6  HisLeuPheMetAspGluIleThrMetAspProLeuHisAlaValTyr---LeuThrVal  24
              |||          :::                  |||            :::  |||||||
Db   2621056  CACTTCTTGCAAGAGAACGCAGCCATGCATGGTCTCTCTATTATTTCATACTGACCGTG  2621115

Qy        25  GlyLeuPheValIleThrPhePheAsnProGlyAlaAsnLeuPheValValGlnThr  44
              :::|||||             :::|||||   :::                |||||
Db   2621116  CTGATGTTTAGCATC--------AGTCCGGGCCAGCCATGATGTTTGCTTCAGCAA  2621166

Qy        45  SerLeuAlaSerGlyArgArgAlaGlyValValThrGlyLeuGlyValAlaLeuGlyAsp  64
              |||        :::        |||  |||||                     :::|||
Db   2621167  TCCCAGAAGAACGGGGTTAAAACTGGTCTCGGCTGCCAGTGCTTGGGACTGAGATTGGCGTA  2621226

Qy        65  AlaPheTyrSerGlyLeuGlyLeuPheGlyLeuAlaThrLeuIleThrGlnCysGluGlu  84
              |||        |||       |||:::::|||:::::::     :::
Db   2621227  TTTATTTACGTCATCCTCACCGCATTGGGTATCAGTACTCGTTTTAAAAGAATACCCATCC  2621286

Qy        85  IlePheSerLeuIleArgIleValGlyGlyValAlaTyrLeuLeuTrpPheAlaTrpCysSer  104
              |||:::     :::|||  ::::::|||||||||||  :::     |||:::
Db   2621287  ATTTATACCGGCCTGCAAGGGATAGTGCGCCTATCTGCTTTACATCGGCTACCTCAGC  2621346

Qy       105  MetArgArgGlnSer---------ThrProGlnMetSerThrLeuGlnGlnProIle  120
              |||||||:::            |||
Db   2621347  TGGCCCCGTCAGAATGCTTCAAACCAGACTCCTACAGCGTCC---------------  2621388

Qy       121  SerAlaProTrpTyrValPhePheArgArgGlyLeuIleThrAspLeuSerAsnProGln  140
              :::  :::             |||  :::|||:::::    :::|||||||:::
Db   2621389  CGTTCAAGTTACACAGGCACCTTCATACAAGGAGTGCTGATTAACCTGACGAATCCCAAG  2621448

Qy       141  ThrValLeuPhePheSerIle  148
              |||||||||||:::|||:::
Db   2621449  ATCGTTTTGTTCTTCCTCAGTCTG  2621472
```

Search completed: January 25, 2005, 15:26:48
Job time : 5150 secs